



SEQUENCE LISTING

<110> Haas, Rainer
Kleanthous, Harold
Tomb, Jean-Francois
Miller, Charles
Al-Garawi, Amal
Odenbreit, Stefan
Meyer, Thomas

<120> Helicobacter Polypeptides and
Corresponding Polynucleotide Molecules

<130> 06132/040002

<140> US 09/988,067

<141> 2001-11-16

<150> US 08/831,309

<151> 1997-04-01

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Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser
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tgg gta ggg acg att gtt att gtg ctg ttg gtt atc ttt ttt atc gcg 157
Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala
15 20 25

caa gcc ttt atc att ccc tct cgc tct atg gtt ggc acg ctc tat gag 205
Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu
30 35 40 45

ggc gac atg ctc ttt gtc aaa aag ttt tct tac ggc ata ccc att cct 253
Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro
50 55 60

aaa atc cca tgg att gag ctt cct gtt atg cct gat ttt aaa aat aac 301
Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn
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Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val	
80 85 90	
ttt atc cct ccc cat gaa aaa aag tct tac tat gtt aaa agg aat ttt	397
Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe	
95 100 105	
gcc att gga ggc gat gag gtg ttg ttc act aat gag ggt ttt tat ttg	445
Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu	
110 115 120 125	
cac cct ttt gag agc gac acg gac aaa aat tac atc gct aaa cat tac	493
His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr	
130 135 140	
cct aac gcc atg aca aaa gaa ttt atg ggt aaa att ttt gtt tta aac	541
Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn	
145 150 155	
cct tat aaa aat gag cat ccg ggt atc cat tac caa aaa gac aat gaa	589
Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu	
160 165 170	
acc ttc cac tta atg gag caa tta gcc act caa ggc gca gaa gct aat	637
Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn	
175 180 185	
atc agc atg caa ctc att caa atg gag ggc gaa aag gtg ttt tat aag	685
Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys	
190 195 200 205	
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Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn	
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Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val	
225 230 235	
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Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu	
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gaa atg gat gca gaa aat aac cct aaa aaa cgc tat ctg gtg cgt tgg	877
Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp	
255 260 265	
gaa cgc atg ttt aaa agc gtt gga ggc tta gaa aaa atc att aaa aaa	925
Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys	
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 35 40 45
 Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro
 50 55 60
 Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu
 65 70 75 80
 Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro
 85 90 95
 Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly
 100 105 110
 Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe
 115 120 125
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 130 135 140
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 145 150 155 160
 Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His
 165 170 175
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 180 185 190
 Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn
 195 200 205
 Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp
 210 215 220
 Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro
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 Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp
 245 250 255
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gca gtg gtt gtt tta ttt tta acg ctg gtt tta ttg ttt tta gtt tta 165
 Ala Val Val Val Leu Phe Leu Thr Leu Val Leu Leu Phe Leu Val Leu
 5 10 15

agg gat ttt ggt tta gca agc ccc aaa caa aag att tta gct ttt tta 213
 Arg Asp Phe Gly Leu Ala Ser Pro Lys Gln Lys Ile Leu Ala Phe Leu
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atc gta ggg att ata gga gcg agc atc agc gtt tat act tac aag caa 261
 Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr Lys Gln
 35 40 45 50

aac caa caa aac caa caa gag atc gct ttg caa aga gcg ttt tta agg 309
 Asn Gln Gln Asn Gln Gln Glu Ile Ala Leu Gln Arg Ala Phe Leu Arg
 55 60 65

ggg gaa acc ttg ttg tgt aaa ggc att aaa gtc aat aac caa acc ttt 357
 Gly Glu Thr Leu Leu Cys Lys Gly Ile Lys Val Asn Asn Gln Thr Phe
 70 75 80

aat tta gtg agc gga act tta agc ttt tta ggc aaa aaa caa acc cct 405
 Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln Thr Pro
 85 90 95

atg aaa gac gtt ctt gtg gat ttg gat tct tgt cag acg ctc caa aaa 453
 Met Lys Asp Val Leu Val Asp Leu Asp Ser Cys Gln Thr Leu Gln Lys
 100 105 110

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Phe Leu Ile Val Gly Ile Ile Gly Ala Ser Ile Ser Val Tyr Thr Tyr
 35 40 45

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 50 55 60

Leu Arg Gly Glu Thr Leu Cys Lys Gly Ile Lys Val Asn Asn Gln
 65 70 75 80

Thr Phe Asn Leu Val Ser Gly Thr Leu Ser Phe Leu Gly Lys Lys Gln
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 aaaccaacga aacc atg aaa aaa gct ctc tta cta act ctc tct ctc tcg 170
 Met Lys Lys Ala Leu Leu Leu Thr Leu Ser Leu Ser
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 ttc tgg ctc cac gct gaa agg aat gga ttt tat tta ggt tta aat ttt 218
 Phe Trp Leu His Ala Glu Arg Asn Gly Phe Tyr Leu Gly Leu Asn Phe
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 cta gaa gga agc tat att aaa gga caa ggt agc atc ggc aaa aaa gct 266
 Leu Glu Gly Ser Tyr Ile Lys Gly Gln Gly Ser Ile Gly Lys Lys Ala
 30 35 40
 tca gca gaa aac gcc tta aat gaa gcg atc aat aac gca aaa aat tca 314
 Ser Ala Glu Asn Ala Leu Asn Glu Ala Ile Asn Asn Ala Lys Asn Ser
 45 50 55 60
 tta ttc cct aac aca aaa gcc ata aga gat gca caa aac gcc tta aat 362
 Leu Phe Pro Asn Thr Lys Ala Ile Arg Asp Ala Gln Asn Ala Leu Asn
 65 70 75
 gca gtg aaa gat tca aac aaa atc gct agc cga ttc gca gga aat ggt 410
 Ala Val Lys Asp Ser Asn Lys Ile Ala Ser Arg Phe Ala Gly Asn Gly
 80 85 90
 gga tcg ggc ggt ctt ttt aat gag ctc agc ttt ggg tat aaa tat ttt 458
 Gly Ser Gly Gly Leu Phe Asn Glu Leu Ser Phe Gly Tyr Lys Tyr Phe
 95 100 105
 ttg ggt aaa aaa agg att ata ggg ttt agg cac tct ctt ttt ttc ggt 506
 Leu Gly Lys Lys Arg Ile Ile Gly Phe Arg His Ser Leu Phe Phe Gly
 110 115 120
 tac caa ctt ggt ggc gtt ggt tct gtt cct ggt agc ggt tta atc gtt 554
 Tyr Gln Leu Gly Gly Val Gly Ser Val Pro Gly Ser Gly Leu Ile Val
 125 130 135 140
 ttt tta ccc tat ggt ttc aat acg gat ttg ctc att aat tgg act aac 602
 Phe Leu Pro Tyr Gly Phe Asn Thr Asp Leu Leu Ile Asn Trp Thr Asn
 145 150 155
 gat aag cga gcg tcc caa aaa tat gtt gaa cga agg gta aaa ggg ctc 650
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 Ser Ile Phe Tyr Lys Asp Met Thr Gly Arg Thr Leu Asp Ala Asn Thr
 175 180 185

tta aaa aaa gca tca agg cat gta ttt aga aaa tct tca ggg ctt gtg 746
 Leu Lys Lys Ala Ser Arg His Val Phe Arg Lys Ser Ser Gly Leu Val
 190 195 200
 att ggc atg gaa cta ggg ggt agc act tgg ttt gca agt aac aat ctc 794
 Ile Gly Met Glu Leu Gly Gly Ser Thr Trp Phe Ala Ser Asn Asn Leu
 205 210 215 220
 acc cct ttc aat caa gtc aag agt cgc acg att ttt cag ttg caa gga 842
 Thr Pro Phe Asn Gln Val Lys Ser Arg Thr Ile Phe Gln Leu Gln Gly
 225 230 235
 aaa ttt ggc gtt cgt tgg aat aat gat gaa tac gat att gat cgc tat 890
 Lys Phe Gly Val Arg Trp Asn Asn Asp Glu Tyr Asp Ile Asp Arg Tyr
 240 245 250
 ggc gat gaa atc tat ctt gga ggt tct agt gtt gaa tta ggg gtt aaa 938
 Gly Asp Glu Ile Tyr Leu Gly Gly Ser Ser Val Glu Leu Gly Val Lys
 255 260 265
 gtg cca gcg ttt aaa gtc aat tac tat agc gat gat tat ggg gat aaa 986
 Val Pro Ala Phe Lys Val Asn Tyr Tyr Ser Asp Asp Tyr Gly Asp Lys
 270 275 280
 ttg gat tat aaa aga gtg gtg agc gtt tat ctt aac tat aca tat aac 1034
 Leu Asp Tyr Lys Arg Val Val Ser Val Tyr Leu Asn Tyr Thr Tyr Asn
 285 290 295 300
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 Phe Lys Asn Lys His
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 Tyr Ile Lys Gly Gln Gly Ser Ile Gly Lys Lys Ala Ser Ala Glu Asn
 35 40 45
 Ala Leu Asn Glu Ala Ile Asn Asn Ala Lys Asn Ser Leu Phe Pro Asn
 50 55 60
 Thr Lys Ala Ile Arg Asp Ala Gln Asn Ala Leu Asn Ala Val Lys Asp
 65 70 75 80
 Ser Asn Lys Ile Ala Ser Arg Phe Ala Gly Asn Gly Gly Ser Gly Gly
 85 90 95
 Leu Phe Asn Glu Leu Ser Phe Gly Tyr Lys Tyr Phe Leu Gly Lys Lys
 100 105 110
 Arg Ile Ile Gly Phe Arg His Ser Leu Phe Phe Gly Tyr Gln Leu Gly
 115 120 125

Gly Val Gly Ser Val Pro Gly Ser Gly Leu Ile Val Phe Leu Pro Tyr
 130 135 140
 Gly Phe Asn Thr Asp Leu Leu Ile Asn Trp Thr Asn Asp Lys Arg Ala
 145 150 155 160
 Ser Gln Lys Tyr Val Glu Arg Arg Val Lys Gly Leu Ser Ile Phe Tyr
 165 170 175
 Lys Asp Met Thr Gly Arg Thr Leu Asp Ala Asn Thr Leu Lys Lys Ala
 180 185 190
 Ser Arg His Val Phe Arg Lys Ser Ser Gly Leu Val Ile Gly Met Glu
 195 200 205
 Leu Gly Gly Ser Thr Trp Phe Ala Ser Asn Asn Leu Thr Pro Phe Asn
 210 215 220
 Gln Val Lys Ser Arg Thr Ile Phe Gln Leu Gln Gly Lys Phe Gly Val
 225 230 235 240
 Arg Trp Asn Asn Asp Glu Tyr Asp Ile Asp Arg Tyr Gly Asp Glu Ile
 245 250 255
 Tyr Leu Gly Gly Ser Ser Val Glu Leu Gly Val Lys Val Pro Ala Phe
 260 265 270
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 His
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 tccaatcaaa cgcctaaaga a atg aaa gtc aag tcc att tct tat gtc ggg 171
 Met Lys Val Lys Ser Ile Ser Tyr Val Gly
 1 5 10
 ctt tct tac atg tct gac atg ctc gct aat gaa att gta aag att cgt 219
 Leu Ser Tyr Met Ser Asp Met Leu Ala Asn Glu Ile Val Lys Ile Arg
 15 20 25
 gtg ggc gat att gtg gat tct aaa aaa ata gac acc gct gtt ttg gct 267
 Val Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala
 30 35 40
 ttg ttc aat caa ggg tat ttt aaa gac gtt tat gcc act ttt gaa ggc 315
 Leu Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly
 45 50 55
 ggc ata tta gag ttt cat ttt gat gaa aaa gcc agg att gcc ggg gta 363
 Gly Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val
 60 65 70
 gaa atc aag ggt tat ggg act gaa aag gaa aaa gac ggc tta aaa tcc 411

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Gln	Met	Gly	Ile	Lys 95	Lys	Gly	Asp	Thr	Phe 100	Asp	Glu	Gln	Lys	Leu 105	Glu	
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His	Ala	Lys	Thr 110	Ala	Leu	Lys	Thr	Ala 115	Leu	Glu	Gly	Gln	Gly	Tyr	Tyr	
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Gly	Ser	Val 125	Val	Glu	Val	Arg	Thr 130	Glu	Lys	Val	Ser	Glu 135	Gly	Ala	Leu	
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Leu	Ile	Val	Phe	Asp	Val	Asn 145	Arg	Gly	Asp	Ser	Ile 150	Tyr	Ile	Lys	Gln	
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Ser	Ile	Tyr	Glu	Gly	Ser 160	Ala	Lys	Leu	Lys	Arg	Arg	Met	Ile	Glu	Ser 170	
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Ser	Pro	Phe	Leu	Lys	Thr	Asp 225	Phe	Ser	Thr	His	Asp 230	Ala	Lys	Leu	His	
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Tyr	Lys	Val	Lys	Glu	Gly 240	Ile	Gln	Tyr	Arg	Ile 245	Ser	Asp	Ile	Leu	Ile 250	
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Glu	Ile	Asp	Asn 255	Pro	Val	Val	Pro	Leu	Lys 260	Thr	Leu	Glu	Lys	Ala 265	Leu	
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Ala	Gln	Ile	Leu	Lys	Thr 285	Glu	Ile	Ala 290	Asp	Lys	Gly	Tyr	Ala	Phe	Ala	
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tcc gaa aat tct tta agg cgt tta gga ttc ttc tct aaa gtc aaa att Ser Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile 365 370 375	1275
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gaa gag ggg cgt act ggg cag ttg caa ttt ggg tta ggc tat ggc tct Glu Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser 395 400 405 410	1371
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caa caa ggc ggg ggc ttt ggg gtg aat gtc ggg cgc atg ctg ggt aat Gln Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn 495 500 505	1659
aga acc cat gtg agc tta ggg tat aac ttg aat gtt acc aaa ctc ctt Arg Thr His Val Ser Leu Gly Tyr Asn Leu Asn Val Thr Lys Leu Leu 510 515 520	1707
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Pro Gly Ala Ile Thr Ser Pro Glu Ile Arg Gly Ile Trp Asp Arg	
575 580 585	
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Asp Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp Val Ser Tyr	
590 595 600	
gac aac acc gat gat tat tac ttc cct aga aat ggg gtt atc ttt agt	1995
Asp Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val Ile Phe Ser	
605 610 615	
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Ser Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr Leu Asn Ser	
620 625 630	
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Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly Lys	
635 640 645 650	
ttc gcc gct tac cac cat ttg caa aaa tat tta ttg ata gat ttg atc	2139
Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu Ile	
655 660 665	
gct cgc ttt aaa acg caa gga ggt tat atc ttt agg tat aac acc gat	2187
Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr Asp	
670 675 680	
gat tac ttg ccc tta aac tcc acc ttc tac atg ggg ggc gta acc acg	2235
Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr	
685 690 695	
gtg aga ggc ttt agg aac gga tgc gtt act cct aaa gat gag ttt ggc	2283
Val Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly	
700 705 710	
ttg tgg ctt gga ggc gat ggg att ttt acc gct tct act gaa ttg agc	2331
Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser	
715 720 725 730	
tat ggg gtg cta aag gcg gct aaa atg cgc tta gcg tgg ttt ttt gac	2379
Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp	
735 740 745	
ttt ggt ttc tta acc ttt aaa acc cca act aga ggg agt ttt ttc tat	2427
Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr	
750 755 760	
aac gct cct gtt acg aca gcg aat ttt aaa gat tat ggc gtt ata ggg	2475
Asn Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly	
765 770 775	
gct ggg ttt gaa aga gcg act tgg agg gct tcc aca ggc ttg cag att	2523
Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile	

780	785	790	
gaa tgg att tcg ccc atg ggg cct ttg gtg ttg att ttc cct ata gcg			2571
Glu Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala			
795	800	805	810
ttt ttc aac caa tgg ggc gat ggc aat ggc aag aaa tgt aaa ggg cta			2619
Phe Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu			
	815	820	825
tgc ttc aac cct aac atg gac gat tac acg caa cac ttt gaa ttt tct			2667
Cys Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser			
	830	835	840
atg gga aca agg ttt taaaatgcgc atcaacagag aagaaatttt ggatttaatg			2722
Met Gly Thr Arg Phe			
	845		
aaaaacgcgc ccttgaaaga attggggcaa agggctttga ggggtgaagca acgcttgcac			2782
cctgaaaact tgacgacttt tattgtggat aggaatatca attacaccaa tatttgtttt			2842
gtggattgca agttttgcgc gttcaaacgc accttaaaag aaaaagacgc ctatgtgttg			2902
agctatgaag aaattgatca aaagattgaa gaattgctcg ctattggcgg cagcgagatc			2962
ctttttcaag ggggggtgca cccgcagcta aagattgatt attatgagaa			3012
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<212> PRT			
<213> Helicobacter pylori			
 <400> 8			
Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu Ser Tyr Met Ser Asp			
1	5	10	15
Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val Gly Asp Ile Val Asp			
	20	25	30
Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu Phe Asn Gln Gly Tyr			
	35	40	45
Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly Ile Leu Glu Phe His			
	50	55	60
Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu Ile Lys Gly Tyr Gly			
	65	70	75
Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln Met Gly Ile Lys Lys			
	85	90	95
Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His Ala Lys Thr Ala Leu			
	100	105	110
Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly Ser Val Val Glu Val			
	115	120	125
Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu Ile Val Phe Asp Val			
	130	135	140
Asn Arg Gly Asp Ser Ile Tyr Ile Lys Gln Ser Ile Tyr Glu Gly Ser			
	145	150	155
Ala Lys Leu Lys Arg Arg Met Ile Glu Ser Leu Ser Ala Asn Lys Gln			
	165	170	175
Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn Asp Gly Lys Leu Arg			
	180	185	190
Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile Gln Asp Val Tyr Met			
	195	200	205
Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser Pro Phe Leu Lys Thr			
	210	215	220
Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr Lys Val Lys Glu Gly			

225	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile	Glu	Ile	Asp	Asn	Pro	Val	240
					245					250						255	
Val	Pro	Leu	Lys	Thr	Leu	Glu	Lys	Ala	Leu	Lys	Val	Lys	Arg	Lys	Asp		
			260					265						270			
Val	Phe	Asn	Ile	Glu	His	Leu	Arg	Ala	Asp	Ala	Gln	Ile	Leu	Lys	Thr		
		275					280					285					
Glu	Ile	Ala	Asp	Lys	Gly	Tyr	Ala	Phe	Ala	Val	Val	Lys	Pro	Asp	Leu		
	290					295					300						
Asp	Lys	Asp	Glu	Lys	Asn	Gly	Leu	Val	Lys	Val	Ile	Tyr	Arg	Ile	Glu		
305					310					315					320		
Val	Gly	Asp	Met	Val	Tyr	Ile	Asn	Asp	Val	Ile	Ile	Ser	Gly	Asn	Gln		
				325					330					335			
Arg	Thr	Ser	Asp	Arg	Ile	Ile	Arg	Arg	Glu	Leu	Leu	Leu	Gly	Pro	Lys		
			340					345					350				
Asp	Lys	Tyr	Asn	Leu	Thr	Lys	Leu	Arg	Asn	Ser	Glu	Asn	Ser	Leu	Arg		
		355					360					365					
Arg	Leu	Gly	Phe	Phe	Ser	Lys	Val	Lys	Ile	Glu	Glu	Lys	Arg	Val	Asn		
	370					375					380						
Ser	Ser	Leu	Met	Asp	Leu	Leu	Val	Ser	Val	Glu	Glu	Gly	Arg	Thr	Gly		
385					390					395					400		
Gln	Leu	Gln	Phe	Gly	Leu	Gly	Tyr	Gly	Ser	Tyr	Gly	Gly	Leu	Met	Leu		
			405					410						415			
Asn	Gly	Ser	Val	Ser	Glu	Arg	Asn	Leu	Phe	Gly	Thr	Gly	Gln	Ser	Met		
			420					425					430				
Ser	Leu	Tyr	Ala	Asn	Ile	Ala	Thr	Gly	Gly	Gly	Arg	Ser	Tyr	Pro	Gly		
		435				440					445						
Met	Pro	Lys	Gly	Ala	Gly	Arg	Met	Phe	Ala	Gly	Asn	Leu	Ser	Leu	Thr		
	450					455				460							
Asn	Pro	Arg	Ile	Phe	Asp	Ser	Trp	Tyr	Ser	Ser	Thr	Ile	Asn	Leu	Tyr		
465					470					475					480		
Ala	Asp	Tyr	Arg	Ile	Ser	Tyr	Gln	Tyr	Ile	Gln	Gln	Gly	Gly	Gly	Phe		
			485						490					495			
Gly	Val	Asn	Val	Gly	Arg	Met	Leu	Gly	Asn	Arg	Thr	His	Val	Ser	Leu		
			500					505					510				
Gly	Tyr	Asn	Leu	Asn	Val	Thr	Lys	Leu	Leu	Gly	Phe	Ser	Ser	Pro	Leu		
		515					520					525					
Tyr	Asn	Arg	Tyr	Tyr	Ser	Ser	Val	Asn	Glu	Val	Val	Ser	Pro	Arg	Gln		
	530				535						540						
Cys	Ser	Thr	Pro	Ala	Ser	Val	Ile	Ile	Asn	Arg	Leu	Ser	Gly	Gly	Lys		
545					550					555					560		
Thr	Pro	Leu	Gln	Pro	Glu	Ser	Cys	Ser	Ser	Pro	Gly	Ala	Ile	Thr	Thr		
			565						570					575			
Ser	Pro	Glu	Ile	Arg	Gly	Ile	Trp	Asp	Arg	Asp	Tyr	His	Thr	Pro	Ile		
			580					585					590				
Thr	Ser	Ser	Phe	Thr	Leu	Asp	Val	Ser	Tyr	Asp	Asn	Thr	Asp	Asp	Tyr		
		595					600					605					
Tyr	Phe	Pro	Arg	Asn	Gly	Val	Ile	Phe	Ser	Ser	Tyr	Ala	Thr	Met	Ser		
	610				615						620						
Gly	Leu	Pro	Ser	Ser	Gly	Thr	Leu	Asn	Ser	Trp	Asn	Gly	Leu	Gly	Gly		
625					630					635					640		
Asn	Val	Arg	Asn	Thr	Lys	Val	Tyr	Gly	Lys	Phe	Ala	Ala	Tyr	His	His		
			645						650					655			
Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	Ile	Ala	Arg	Phe	Lys	Thr	Gln		
			660					665					670				
Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr	Asp	Asp	Tyr	Leu	Pro	Leu	Asn		
		675					680					685					
Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr	Thr	Val	Arg	Gly	Phe	Arg	Asn		
	690					695					700						

Gly	Ser	Val	Thr	Pro	Lys	Asp	Glu	Phe	Gly	Leu	Trp	Leu	Gly	Gly	Asp
705					710					715					720
Gly	Ile	Phe	Thr	Ala	Ser	Thr	Glu	Leu	Ser	Tyr	Gly	Val	Leu	Lys	Ala
				725					730					735	
Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe	Asp	Phe	Gly	Phe	Leu	Thr	Phe
			740					745					750		
Lys	Thr	Pro	Thr	Arg	Gly	Ser	Phe	Phe	Tyr	Asn	Ala	Pro	Val	Thr	Thr
		755					760					765			
Ala	Asn	Phe	Lys	Asp	Tyr	Gly	Val	Ile	Gly	Ala	Gly	Phe	Glu	Arg	Ala
	770					775					780				
Thr	Trp	Arg	Ala	Ser	Thr	Gly	Leu	Gln	Ile	Glu	Trp	Ile	Ser	Pro	Met
785					790					795					800
Gly	Pro	Leu	Val	Leu	Ile	Phe	Pro	Ile	Ala	Phe	Phe	Asn	Gln	Trp	Gly
				805					810					815	
Asp	Gly	Asn	Gly	Lys	Lys	Cys	Lys	Gly	Leu	Cys	Phe	Asn	Pro	Asn	Met
			820					825					830		
Asp	Asp	Tyr	Thr	Gln	His	Phe	Glu	Phe	Ser	Met	Gly	Thr	Arg	Phe	
		835					840					845			

<210> 9
 <211> 1032
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (149)...(913)

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 tagggggggtt tggttatttg tgtttgatta gaatagggtt gtttttaatt ttcttttaag 120
 aggagttttt acttttttta gggttttt atg gat att tat gcg tta tat ata 172
 Met Asp Ile Tyr Ala Leu Tyr Ile
 1 5

gcg ata ggg ctt ttt act ggc att cta tca ggg att ttt ggc att ggt 220
 Ala Ile Gly Leu Phe Thr Gly Ile Leu Ser Gly Ile Phe Gly Ile Gly
 10 15 20

ggg ggg ttg atc att gtc cct atc atg ctc gca acc ggg cat tct ttt 268
 Gly Gly Leu Ile Ile Val Pro Ile Met Leu Ala Thr Gly His Ser Phe
 25 30 35 40

gaa gaa tcc att ggg att tcc att ttg caa atg gcg ctt tca tcg ttc 316
 Glu Glu Ser Ile Gly Ile Ser Ile Leu Gln Met Ala Leu Ser Ser Phe
 45 50 55

gtg ggc tct gtt ttg aat ttc aaa aaa aaa tcg ctt gat ttt tct tta 364
 Val Gly Ser Val Leu Asn Phe Lys Lys Lys Ser Leu Asp Phe Ser Leu
 60 65 70

ggc ttg ttg ata ggg gca ggg ggg ctg ata ggg gcg agt ttt agc gga 412
 Gly Leu Leu Ile Gly Ala Gly Gly Leu Ile Gly Ala Ser Phe Ser Gly
 75 80 85

ttt gtt tta aaa atc gtt tcc agt aaa att tta atg gtt att ttc gcg 460
 Phe Val Leu Lys Ile Val Ser Ser Lys Ile Leu Met Val Ile Phe Ala
 90 95 100

ctt tta gtc gtg tat tct atg atc caa ttt gtt ttg aaa ccc aaa aaa 508
 Leu Leu Val Val Tyr Ser Met Ile Gln Phe Val Leu Lys Pro Lys Lys
 105 110 115 120

aaa gat ttg ata gcg gat act aaa cgc tat cat ctg caa ggt ttg aaa 556
 Lys Asp Leu Ile Ala Asp Thr Lys Arg Tyr His Leu Gln Gly Leu Lys
 125 130 135

tta ttt tta att ggc acg ctc aca ggg ttt ttt gct atc act tta ggg 604
 Leu Phe Leu Ile Gly Thr Leu Thr Gly Phe Phe Ala Ile Thr Leu Gly
 140 145 150

att ggt ggg ggg atg ctc atg gtg cct ttg atg cat tat ttt tta ggg 652
 Ile Gly Gly Gly Met Leu Met Val Pro Leu Met His Tyr Phe Leu Gly
 155 160 165

tat gat tct aaa aaa tgc gtg gct cta ggg tta ttt ttc atc ttg ttt 700
 Tyr Asp Ser Lys Lys Cys Val Ala Leu Gly Leu Phe Phe Ile Leu Phe
 170 175 180

tct tct att tca gga gct ttt tct tta atg tat cac cac atc atc aat 748
 Ser Ser Ile Ser Gly Ala Phe Ser Leu Met Tyr His His Ile Ile Asn
 185 190 195 200

aaa gaa gtg ctc tta gca ggg gcg att gtg gga tta gga tct gtt atg 796
 Lys Glu Val Leu Leu Ala Gly Ala Ile Val Gly Leu Gly Ser Val Met
 205 210 215

ggc gtg agc att ggg att aaa tgg atc atg ggg ctt ttg aat gaa aaa 844
 Gly Val Ser Ile Gly Ile Lys Trp Ile Met Gly Leu Leu Asn Glu Lys
 220 225 230

atg cat aaa gct ttg att tta ggg gtg tat ggt ttg tcg cta ttg att 892
 Met His Lys Ala Leu Ile Leu Gly Val Tyr Gly Leu Ser Leu Leu Ile
 235 240 245

gtt tta tac aaa ctc ttt ttt taattgatgg ttttatacca ctactatattt 943
 Val Leu Tyr Lys Leu Phe Phe
 250 255

aagacccta agagtttccc tttagagtat ttgcatttgt ggcctaata gagccattta 1003
 ttgagattgg attttgatgc ggccaattt 1032

<210> 10
 <211> 255
 <212> PRT
 <213> Helicobacter pylori

<400> 10
 Met Asp Ile Tyr Ala Leu Tyr Ile Ala Ile Gly Leu Phe Thr Gly Ile
 1 5 10 15
 Leu Ser Gly Ile Phe Gly Ile Gly Gly Leu Ile Ile Val Pro Ile
 20 25 30
 Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile
 35 40 45
 Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys
 50 55 60
 Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly

65	70	75	80
Leu Ile Gly Ala Ser	Phe Ser Gly Phe Val	Leu Lys Ile Val	Ser Ser
	85	90	95
Lys Ile Leu Met Val	Ile Phe Ala Leu	Leu Val Val Tyr	Ser Met Ile
	100	105	110
Gln Phe Val Leu Lys	Pro Lys Lys Lys	Asp Leu Ile Ala	Asp Thr Lys
	115	120	125
Arg Tyr His Leu Gln	Gly Leu Lys Leu	Phe Leu Ile Gly	Thr Leu Thr
	130	135	140
Gly Phe Phe Ala Ile	Thr Leu Gly Ile	Gly Gly Met Leu	Met Val
145	150	155	160
Pro Leu Met His Tyr	Phe Leu Gly Tyr	Asp Ser Lys Lys	Cys Val Ala
	165	170	175
Leu Gly Leu Phe Phe	Ile Leu Phe Ser	Ser Ile Ser Gly	Ala Phe Ser
	180	185	190
Leu Met Tyr His His	Ile Ile Asn Lys	Glu Val Leu Leu	Ala Gly Ala
	195	200	205
Ile Val Gly Leu Gly	Ser Val Met Gly	Val Ser Ile Gly	Ile Lys Trp
	210	215	220
Ile Met Gly Leu Leu	Asn Glu Lys Met	His Lys Ala Leu	Ile Leu Gly
225	230	235	240
Val Tyr Gly Leu Ser	Leu Leu Ile Val	Leu Tyr Lys Leu	Phe Phe
	245	250	255

<210> 11
 <211> 1057
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (66)...(980)

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 ccgtt atg ggt aga att gaa tca aaa aag cgt ttg aaa gcg ctt gtt ttt 110
 Met Gly Arg Ile Glu Ser Lys Lys Arg Leu Lys Ala Leu Val Phe
 1 5 10 15

 tta gcc agc ttg ggg gtt ttg tgg ggc aat agc gct gaa aaa acg cct 158
 Leu Ala Ser Leu Gly Val Leu Trp Gly Asn Ser Ala Glu Lys Thr Pro
 20 25 30

 ttt ttt aaa acg aaa aac cac att tat cta ggt ttt agg cta ggc aca 206
 Phe Phe Lys Thr Lys Asn His Ile Tyr Leu Gly Phe Arg Leu Gly Thr
 35 40 45

 gga gcc aat gtg cac acg agc atg tgg caa caa gcc tat aaa gac aac 254
 Gly Ala Asn Val His Thr Ser Met Trp Gln Gln Ala Tyr Lys Asp Asn
 50 55 60

 ccc acc tgc cct ggt agc gtg tgt tat ggc gag aaa tta gaa gcc cat 302
 Pro Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His
 65 70 75

 tat cag ggg ggt aaa aac ctg tct tat acc ggg caa ata ggc gat gaa 350
 Tyr Gln Gly Gly Lys Asn Leu Ser Tyr Thr Gly Gln Ile Gly Asp Glu
 80 85 90 95

ata gct ttt gat aaa cac cat att tta ggc tta agg gtg tgg ggg gat	398
Ile Ala Phe Asp Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp	
100 105 110	
gta gaa tac gct aaa gcg caa tta ggt caa aaa gtg ggg ggt aat acc	446
Val Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr	
115 120 125	
ctt tta tcc caa gcc aat tat gac cca aac gcg att aaa acc tac gat	494
Leu Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp	
130 135 140	
tct gct tca aac act caa ggc cct tta gtt ttg caa aaa acc cca agc	542
Ser Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser	
145 150 155	
cct caa aac ttc ctt ttc aat aac ggg cat ttc atg gcg ttt ggt ttg	590
Pro Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu	
160 165 170 175	
aac gtg aat gtg ttt gtt aac ctc cct ata gac acc ctt tta aaa ctc	638
Asn Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu	
180 185 190	
gct tta aaa aca gaa aaa atg ctg ttt ttt aaa ata ggc gtg ttt ggt	686
Ala Leu Lys Thr Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly	
195 200 205	
ggg ggc ggg gtg gaa tac gca ata tta tgg agt cct aac tat caa aat	734
Gly Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn	
210 215 220	
caa aac acg aaa caa ggc gat aaa ttt ttt gca gcg ggt ggg ggg ttt	782
Gln Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe	
225 230 235	
ttt gtg aat ttt ggg ggt tct ttg tat ata ggc aaa cgc aac cgc ttc	830
Phe Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe	
240 245 250 255	
aat gtg ggg tta aaa atc cct tac tat agc ttg agc gcg caa agt tgg	878
Asn Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp	
260 265 270	
aaa aac ttt ggc tct agc aat gtg tgg cag caa caa acg atc cga caa	926
Lys Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln	
275 280 285	
aac ttc agc gtt ttt agg aat aaa gaa gtt ttt gtc agc tac gcg ttc	974
Asn Phe Ser Val Phe Arg Asn Lys Glu Val Phe Val Ser Tyr Ala Phe	
290 295 300	
ttg ttt tagtttggat tcgtttctcat taaacactga tgataaaatt caaaagatgg	1030
Leu Phe	
305	
ttttatcggtt acaaaattca acatttc	1057

<210> 12
 <211> 305
 <212> PRT
 <213> Helicobacter pylori

<400> 12
 Met Gly Arg Ile Glu Ser Lys Lys Arg Leu Lys Ala Leu Val Phe Leu
 1 5 10 15
 Ala Ser Leu Gly Val Leu Trp Gly Asn Ser Ala Glu Lys Thr Pro Phe
 20 25 30
 Phe Lys Thr Lys Asn His Ile Tyr Leu Gly Phe Arg Leu Gly Thr Gly
 35 40 45
 Ala Asn Val His Thr Ser Met Trp Gln Gln Ala Tyr Lys Asp Asn Pro
 50 55 60
 Thr Cys Pro Gly Ser Val Cys Tyr Gly Glu Lys Leu Glu Ala His Tyr
 65 70 75 80
 Gln Gly Gly Lys Asn Leu Ser Tyr Thr Gly Gln Ile Gly Asp Glu Ile
 85 90 95
 Ala Phe Asp Lys His His Ile Leu Gly Leu Arg Val Trp Gly Asp Val
 100 105 110
 Glu Tyr Ala Lys Ala Gln Leu Gly Gln Lys Val Gly Gly Asn Thr Leu
 115 120 125
 Leu Ser Gln Ala Asn Tyr Asp Pro Asn Ala Ile Lys Thr Tyr Asp Ser
 130 135 140
 Ala Ser Asn Thr Gln Gly Pro Leu Val Leu Gln Lys Thr Pro Ser Pro
 145 150 155 160
 Gln Asn Phe Leu Phe Asn Asn Gly His Phe Met Ala Phe Gly Leu Asn
 165 170 175
 Val Asn Val Phe Val Asn Leu Pro Ile Asp Thr Leu Leu Lys Leu Ala
 180 185 190
 Leu Lys Thr Glu Lys Met Leu Phe Phe Lys Ile Gly Val Phe Gly Gly
 195 200 205
 Gly Gly Val Glu Tyr Ala Ile Leu Trp Ser Pro Asn Tyr Gln Asn Gln
 210 215 220
 Asn Thr Lys Gln Gly Asp Lys Phe Phe Ala Ala Gly Gly Gly Phe Phe
 225 230 235 240
 Val Asn Phe Gly Gly Ser Leu Tyr Ile Gly Lys Arg Asn Arg Phe Asn
 245 250 255
 Val Gly Leu Lys Ile Pro Tyr Tyr Ser Leu Ser Ala Gln Ser Trp Lys
 260 265 270
 Asn Phe Gly Ser Ser Asn Val Trp Gln Gln Gln Thr Ile Arg Gln Asn
 275 280 285
 Phe Ser Val Phe Arg Asn Lys Glu Val Phe Val Ser Tyr Ala Phe Leu
 290 295 300
 Phe
 305

<210> 13
 <211> 624
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (77)...(535)

<400> 13
 tattagttgg ttttaacgc tataatctgt gtgccaat tgtgtggctc aaatcatttt 60

taaaaggggt tttata atg gaa aac aac gaa aat cat gag aaa ttg aat ggc 112
 Met Glu Asn Asn Glu Asn His Glu Lys Leu Asn Gly
 1 5 10

gtt ttg cgc aag ttt tta ggc gat gcg ttc acg ctt gat ggg aaa gaa 160
 Val Leu Arg Lys Phe Leu Gly Asp Ala Phe Thr Leu Asp Gly Lys Glu
 15 20 25

gga gga ttg aat atg gaa aaa ttg cgc gaa gcc att aaa aaa gaa aaa 208
 Gly Gly Leu Asn Met Glu Lys Leu Arg Glu Ala Ile Lys Lys Glu Lys
 30 35 40

cca atc atg aat att ttg ctc atg gga gct act ggg gtg ggt aaa agc 256
 Pro Ile Met Asn Ile Leu Leu Met Gly Ala Thr Gly Val Gly Lys Ser
 45 50 55 60

tgc ctc att aac gct cta ttc ggt aag gaa gta gct aaa gca ggt gta 304
 Ser Leu Ile Asn Ala Leu Phe Gly Lys Glu Val Ala Lys Ala Gly Val
 65 70 75

gga aaa ccc atc act cag cat ctt gaa aaa tat gtt gat gaa gaa aaa 352
 Gly Lys Pro Ile Thr Gln His Leu Glu Lys Tyr Val Asp Glu Glu Lys
 80 85 90

ggc ttg att tta tgg gac act aaa ggc att gaa gat aaa gat tat gaa 400
 Gly Leu Ile Leu Trp Asp Thr Lys Gly Ile Glu Asp Lys Asp Tyr Glu
 95 100 105

aat acc ttg gaa agc att aaa aaa gaa atg gaa gat tct ttt aaa acg 448
 Asn Thr Leu Glu Ser Ile Lys Lys Glu Met Glu Asp Ser Phe Lys Thr
 110 115 120

ctt gat gaa aaa gag gct att gat gtg gcg tat ctg tgc gtt aaa gag 496
 Leu Asp Glu Lys Glu Ala Ile Asp Val Ala Tyr Leu Cys Val Lys Glu
 125 130 135 140

act tct ggt agg gtt caa gag aga gag aga gag agt tat taagctttac 545
 Thr Ser Gly Arg Val Gln Glu Arg Glu Arg Glu Ser Tyr
 145 150

taaaaaatgg aatatcccaa cgattttcgt tttcaccaac acacaagaaa aagccggcga 605
 tgcctttgtt aaaaaaact 624

<210> 14
 <211> 153
 <212> PRT
 <213> Helicobacter pylori

<400> 14
 Met Glu Asn Asn Glu Asn His Glu Lys Leu Asn Gly Val Leu Arg Lys
 1 5 10 15
 Phe Leu Gly Asp Ala Phe Thr Leu Asp Gly Lys Glu Gly Gly Leu Asn
 20 25 30
 Met Glu Lys Leu Arg Glu Ala Ile Lys Lys Glu Lys Pro Ile Met Asn
 35 40 45
 Ile Leu Leu Met Gly Ala Thr Gly Val Gly Lys Ser Ser Leu Ile Asn
 50 55 60
 Ala Leu Phe Gly Lys Glu Val Ala Lys Ala Gly Val Gly Lys Pro Ile
 65 70 75 80

Thr	Gln	His	Leu	Glu	Lys	Tyr	Val	Asp	Glu	Glu	Lys	Gly	Leu	Ile	Leu
			85					90						95	
Trp	Asp	Thr	Lys	Gly	Ile	Glu	Asp	Lys	Asp	Tyr	Glu	Asn	Thr	Leu	Glu
			100					105					110		
Ser	Ile	Lys	Lys	Glu	Met	Glu	Asp	Ser	Phe	Lys	Thr	Leu	Asp	Glu	Lys
		115					120					125			
Glu	Ala	Ile	Asp	Val	Ala	Tyr	Leu	Cys	Val	Lys	Glu	Thr	Ser	Gly	Arg
	130					135					140				
Val	Gln	Glu	Arg	Glu	Arg	Glu	Ser	Tyr							
145					150										

<210> 15
 <211> 1083
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (155)...(1033)

<400> 15
 gatgttggtta agtcgttggtt tattatgtta cactaaaagc ttaaataaaa gggcataagg 60
 gataaaggga gtgttagtag atagttttta taggggttatt gactatatta gggtttctgt 120
 aaccaaacag tgcaatttca ggtgtcagta ttgc atg cct gct acg cca tta aat 175
 Met Pro Ala Thr Pro Leu Asn
 1 5

ttt	ttt	gat	aat	gaa	gaa	tta	ttg	cct	ttg	gat	aat	ggt	tta	gaa	ttt	223
Phe	Phe	Asp	Asn	Glu	Glu	Leu	Leu	Pro	Leu	Asp	Asn	Val	Leu	Glu	Phe	
		10					15					20				

ctc	aaa	atc	gcc	att	gat	gag	ggc	ggt	aaa	aaa	att	aga	atc	acg	ggg	271
Leu	Lys	Ile	Ala	Ile	Asp	Glu	Gly	Val	Lys	Lys	Ile	Arg	Ile	Thr	Gly	
	25					30					35					

ggg	gag	ccg	cta	tta	cgc	aaa	ggc	tta	gat	gaa	ttt	atc	gct	aaa	ttg	319
Gly	Glu	Pro	Leu	Leu	Arg	Lys	Gly	Leu	Asp	Glu	Phe	Ile	Ala	Lys	Leu	
40					45				50					55		

cac	gct	tac	aat	aaa	gaa	gtg	gag	tta	ggt	tta	agc	act	aat	ggg	ttt	367
His	Ala	Tyr	Asn	Lys	Glu	Val	Glu	Leu	Val	Leu	Ser	Thr	Asn	Gly	Phe	
			60					65						70		

tta	ctc	aaa	aaa	atg	gct	aag	gat	tta	aaa	aat	gcc	ggg	tta	gcg	caa	415
Leu	Leu	Lys	Lys	Met	Ala	Lys	Asp	Leu	Lys	Asn	Ala	Gly	Leu	Ala	Gln	
			75					80					85			

gtg	aat	ggt	tca	ttg	gat	tct	tta	aaa	agc	gat	agg	ggt	tta	aaa	atc	463
Val	Asn	Val	Ser	Leu	Asp	Ser	Leu	Lys	Ser	Asp	Arg	Val	Leu	Lys	Ile	
	90					95						100				

tct	caa	aaa	gac	gct	ctt	aaa	aac	acg	cta	gaa	ggg	att	gaa	gag	tct	511
Ser	Gln	Lys	Asp	Ala	Leu	Lys	Asn	Thr	Leu	Glu	Gly	Ile	Glu	Glu	Ser	
	105					110					115					

ttg	aaa	gtg	ggg	tta	aaa	ctc	aaa	tta	aac	acg	ggt	gtg	ata	aaa	agc	559
Leu	Lys	Val	Gly	Leu	Lys	Leu	Lys	Leu	Asn	Thr	Val	Val	Ile	Lys	Ser	
120					125					130					135	

gtt aat gat gat gaa atc tta gag ctt tta gaa tac gca aaa aat agg 607
 Val Asn Asp Asp Glu Ile Leu Glu Leu Leu Glu Tyr Ala Lys Asn Arg
 140 145 150
 cat ata caa atc cgc tac att gaa ttt atg gaa aac acg cat gct aaa 655
 His Ile Gln Ile Arg Tyr Ile Glu Phe Met Glu Asn Thr His Ala Lys
 155 160 165
 agt ttg gtt aaa ggc ttg aaa gag cga gaa att tta gat ttg atc gct 703
 Ser Leu Val Lys Gly Leu Lys Glu Arg Glu Ile Leu Asp Leu Ile Ala
 170 175 180
 caa aaa tat caa atc att gag gca gaa aaa ccc aaa caa ggg tct tct 751
 Gln Lys Tyr Gln Ile Ile Glu Ala Glu Lys Pro Lys Gln Gly Ser Ser
 185 190 195
 aaa atc tac acg cta gaa aat ggc tat caa ttt ggc att atc gct ccg 799
 Lys Ile Tyr Thr Leu Glu Asn Gly Tyr Gln Phe Gly Ile Ile Ala Pro
 200 205 210 215
 cat agc gat gat ttt tgc caa tct tgc aat cgt atc cgt ttg gct tct 847
 His Ser Asp Asp Phe Cys Gln Ser Cys Asn Arg Ile Arg Leu Ala Ser
 220 225 230
 gat ggt aag att tgc cca tgt tta tac tat caa gac gcc ata gac gct 895
 Asp Gly Lys Ile Cys Pro Cys Leu Tyr Tyr Gln Asp Ala Ile Asp Ala
 235 240 245
 aaa gag gcg atc atc aat aag gat aca aaa aat ata aaa agg ctt tta 943
 Lys Glu Ala Ile Ile Asn Lys Asp Thr Lys Asn Ile Lys Arg Leu Leu
 250 255 260
 aag caa tct gtc atc aat aaa cca gaa aaa aac atg tgg aat gat aaa 991
 Lys Gln Ser Val Ile Asn Lys Pro Glu Lys Asn Met Trp Asn Asp Lys
 265 270 275
 aac agc gaa act ccc aca agg gcg ttt tac tac aca ggg ggg 1033
 Asn Ser Glu Thr Pro Thr Arg Ala Phe Tyr Tyr Thr Gly Gly
 280 285 290
 taggggagta aaatatttat tattttaaac ctttttatta aaaataaggc 1083

<210> 16
 <211> 293
 <212> PRT
 <213> Helicobacter pylori

<400> 16
 Met Pro Ala Thr Pro Leu Asn Phe Phe Asp Asn Glu Glu Leu Leu Pro
 1 5 10 15
 Leu Asp Asn Val Leu Glu Phe Leu Lys Ile Ala Ile Asp Glu Gly Val
 20 25 30
 Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu Leu Arg Lys Gly Leu
 35 40 45
 Asp Glu Phe Ile Ala Lys Leu His Ala Tyr Asn Lys Glu Val Glu Leu
 50 55 60
 Val Leu Ser Thr Asn Gly Phe Leu Leu Lys Lys Met Ala Lys Asp Leu
 65 70 75 80

Lys Asn Ala Gly Leu Ala Gln Val Asn Val Ser Leu Asp Ser Leu Lys
 85 90 95
 Ser Asp Arg Val Leu Lys Ile Ser Gln Lys Asp Ala Leu Lys Asn Thr
 100 105 110
 Leu Glu Gly Ile Glu Glu Ser Leu Lys Val Gly Leu Lys Leu Lys Leu
 115 120 125
 Asn Thr Val Val Ile Lys Ser Val Asn Asp Asp Glu Ile Leu Glu Leu
 130 135 140
 Leu Glu Tyr Ala Lys Asn Arg His Ile Gln Ile Arg Tyr Ile Glu Phe
 145 150 155 160
 Met Glu Asn Thr His Ala Lys Ser Leu Val Lys Gly Leu Lys Glu Arg
 165 170 175
 Glu Ile Leu Asp Leu Ile Ala Gln Lys Tyr Gln Ile Ile Glu Ala Glu
 180 185 190
 Lys Pro Lys Gln Gly Ser Ser Lys Ile Tyr Thr Leu Glu Asn Gly Tyr
 195 200 205
 Gln Phe Gly Ile Ile Ala Pro His Ser Asp Asp Phe Cys Gln Ser Cys
 210 215 220
 Asn Arg Ile Arg Leu Ala Ser Asp Gly Lys Ile Cys Pro Cys Leu Tyr
 225 230 235 240
 Tyr Gln Asp Ala Ile Asp Ala Lys Glu Ala Ile Ile Asn Lys Asp Thr
 245 250 255
 Lys Asn Ile Lys Arg Leu Leu Lys Gln Ser Val Ile Asn Lys Pro Glu
 260 265 270
 Lys Asn Met Trp Asn Asp Lys Asn Ser Glu Thr Pro Thr Arg Ala Phe
 275 280 285
 Tyr Tyr Thr Gly Gly
 290

<210> 17
 <211> 1181
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (121)...(1137)

<400> 17
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 tacgattaca aagatgtttt tgggtttaag gcggggcgct atgaagcgaa tattgatttc 120
 atg agc gga tcg aat caa ggg tgg gaa gtg tat tat cag ccc tat aag 168
 Met Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys
 1 5 10 15

 act gaa acg caa agg tta agg ttt tgg tgg tgg agt tct ttt ggg aga 216
 Thr Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg
 20 25 30

 ggt tta gcg ttc aac tct tgg att tat gag ttt ttt gcg acg gtg cct 264
 Gly Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro
 35 40 45

 tat ttg aaa aag gga ggc aat cct aat aac agc aac gat ttc atc aat 312
 Tyr Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn
 50 55 60

 tat ggc tgg cat gga atc acc aca acc tat tct tat aaa ggt tta gac 360

Tyr	Gly	Trp	His	Gly	Ile	Thr	Thr	Thr	Tyr	Ser	Tyr	Lys	Gly	Leu	Asp	
65					70					75					80	
gct	caa	ttt	ttt	tat	tat	ttt	gcg	cct	aag	act	tat	aac	gct	cct	ggc	408
Ala	Gln	Phe	Phe	Tyr	Tyr	Phe	Ala	Pro	Lys	Thr	Tyr	Asn	Ala	Pro	Gly	
				85					90					95		
ttt	aag	ctg	gtc	tat	gac	acg	aat	agg	aat	ttt	caa	aat	gta	ggc	ttt	456
Phe	Lys	Leu	Val	Tyr	Asp	Thr	Asn	Arg	Asn	Phe	Gln	Asn	Val	Gly	Phe	
			100					105					110			
cgc	tct	caa	agc	atg	atc	atg	aca	acc	ttt	cct	tta	tac	tat	aga	ggg	504
Arg	Ser	Gln	Ser	Met	Ile	Met	Thr	Thr	Phe	Pro	Leu	Tyr	Tyr	Arg	Gly	
			115				120					125				
tgg	tat	aac	cca	gag	aca	aac	act	tat	agt	tta	gaa	gac	agc	acg	cct	552
Trp	Tyr	Asn	Pro	Glu	Thr	Asn	Thr	Tyr	Ser	Leu	Glu	Asp	Ser	Thr	Pro	
	130					135					140					
cat	ggc	tcg	ttg	ttg	ggg	agg	aat	ggc	gtt	act	tta	aat	atc	cgc	cag	600
His	Gly	Ser	Leu	Leu	Gly	Arg	Asn	Gly	Val	Thr	Leu	Asn	Ile	Arg	Gln	
145					150				155						160	
gtt	ttt	tgg	tgg	gat	aat	ttc	aac	tgg	tcc	att	ggc	ttt	tat	aac	acc	648
Val	Phe	Trp	Trp	Asp	Asn	Phe	Asn	Trp	Ser	Ile	Gly	Phe	Tyr	Asn	Thr	
				165				170						175		
ttt	ggc	aat	tcg	gac	gct	ttt	tta	ggc	tct	cac	acg	atg	cca	agg	ggg	696
Phe	Gly	Asn	Ser	Asp	Ala	Phe	Leu	Gly	Ser	His	Thr	Met	Pro	Arg	Gly	
			180					185					190			
aat	aac	act	tcc	tat	atc	ggt	agt	gaa	atc	tcc	ata	acg	act	agg	cat	744
Asn	Asn	Thr	Ser	Tyr	Ile	Gly	Ser	Glu	Ile	Ser	Ile	Thr	Thr	Arg	His	
			195				200					205				
gcc	gga	atg	att	ggc	tat	gat	ttt	tgg	gat	aat	acg	gct	tat	gat	ggg	792
Ala	Gly	Met	Ile	Gly	Tyr	Asp	Phe	Trp	Asp	Asn	Thr	Ala	Tyr	Asp	Gly	
	210					215					220					
cta	gct	gat	gcg	atc	act	aac	gct	aac	act	ttc	act	ttt	tac	act	tct	840
Leu	Ala	Asp	Ala	Ile	Thr	Asn	Ala	Asn	Thr	Phe	Thr	Phe	Tyr	Thr	Ser	
225					230					235					240	
gtt	gga	ggg	atc	cat	aag	cgt	ttt	gca	tgg	cat	gtt	ttt	ggg	cgc	gtc	888
Val	Gly	Gly	Ile	His	Lys	Arg	Phe	Ala	Trp	His	Val	Phe	Gly	Arg	Val	
				245					250					255		
tct	cat	gcg	aat	aaa	aac	gcg	tta	ggg	caa	gtg	ggg	agg	gct	aat	gaa	936
Ser	His	Ala	Asn	Lys	Asn	Ala	Leu	Gly	Gln	Val	Gly	Arg	Ala	Asn	Glu	
			260					265					270			
tat	tcc	ttg	caa	ttc	aac	gcg	agc	tat	gcg	ttc	act	gaa	tca	atc	ctt	984
Tyr	Ser	Leu	Gln	Phe	Asn	Ala	Ser	Tyr	Ala	Phe	Thr	Glu	Ser	Ile	Leu	
		275					280					285				
ctt	aac	ttt	agg	atc	act	tat	tat	ggg	gct	agg	atc	aat	aaa	ggg	tat	1032
Leu	Asn	Phe	Arg	Ile	Thr	Tyr	Tyr	Gly	Ala	Arg	Ile	Asn	Lys	Gly	Tyr	
	290					295					300					

caa gcg ggg tat ttt gga gcg ccc aaa ttc aat aac cct gat ggc gat 1080
 Gln Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp
 305 310 315 320

ttt agc gct aat tac caa gac aga agt tac atg atg acc aac ctc acg 1128
 Phe Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr
 325 330 335

ctg aag ttt tgatttccaa tcacagcgag ttaaaaacac tccaaggcat 1177
 Leu Lys Phe

tttt 1181

<210> 18
 <211> 339
 <212> PRT
 <213> Helicobacter pylori

<400> 18
 Met Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys
 1 5 10 15
 Thr Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg
 20 25 30
 Gly Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro
 35 40 45
 Tyr Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn
 50 55 60
 Tyr Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp
 65 70 75 80
 Ala Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly
 85 90 95
 Phe Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe
 100 105 110
 Arg Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly
 115 120 125
 Trp Tyr Asn Pro Glu Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro
 130 135 140
 His Gly Ser Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln
 145 150 155 160
 Val Phe Trp Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr
 165 170 175
 Phe Gly Asn Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly
 180 185 190
 Asn Asn Thr Ser Tyr Ile Gly Ser Glu Ile Ser Ile Thr Thr Arg His
 195 200 205
 Ala Gly Met Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly
 210 215 220
 Leu Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser
 225 230 235 240
 Val Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val
 245 250 255
 Ser His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu
 260 265 270
 Tyr Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu
 275 280 285
 Leu Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr
 290 295 300
 Gln Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp

305 310 315 320
Phe Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr
 325 330 335
Leu Lys Phe

<210> 19
<211> 959
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (133)...(879)

<400> 19
taaggaaatg agtttttata tcataaaata aagtaaccga gaaaaatctt tctctaaaaa 60
taataactttt ttagttataa taacaatttt gttttttcaa aaacaataat tactatatatt 120
aggatttttaa ga atg aat gac aag cgt ttt aga aaa tat tgt agt ttt tct 171
 Met Asn Asp Lys Arg Phe Arg Lys Tyr Cys Ser Phe Ser
 1 5 10

att ttt ttg tcc tta tta gga acg ttt gaa tta gag gct aaa gaa gaa 219
Ile Phe Leu Ser Leu Leu Gly Thr Phe Glu Leu Glu Ala Lys Glu Glu
 15 20 25

gaa gaa aaa gaa gaa aga aag aca gaa agg aaa aaa gaa aag aac gcc 267
Glu Glu Lys Glu Glu Arg Lys Thr Glu Arg Lys Lys Glu Lys Asn Ala
 30 35 40 45

caa cac act cta ggc aag gtt acc act caa gcg gct aaa atc ttt aac 315
Gln His Thr Leu Gly Lys Val Thr Thr Gln Ala Ala Lys Ile Phe Asn
 50 55 60

tac aac aac cag aca acc att tca agt aag gaa tta gaa aga agg caa 363
Tyr Asn Asn Gln Thr Thr Ile Ser Ser Lys Glu Leu Glu Arg Arg Gln
 65 70 75

gcc aac caa atc agc gac atg ttt aga aga aac cct aat atc aat gtg 411
Ala Asn Gln Ile Ser Asp Met Phe Arg Arg Asn Pro Asn Ile Asn Val
 80 85 90

ggc ggt ggt gcg gtg ata gcg caa aaa att tat gtg cgc ggt att gaa 459
Gly Gly Gly Ala Val Ile Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu
 95 100 105

gac aga ttg gct cgg gtt acg gtg gat ggg gcg gcg caa atg ggt gca 507
Asp Arg Leu Ala Arg Val Thr Val Asp Gly Ala Ala Gln Met Gly Ala
 110 115 120 125

agc tat ggg cat caa ggc aat acg atc att gac cct gga atg ctt aaa 555
Ser Tyr Gly His Gln Gly Asn Thr Ile Ile Asp Pro Gly Met Leu Lys
 130 135 140

agc gtg gtg gtt act aaa ggg gcg gct caa gcg agc gcg ggg cct atg 603
Ser Val Val Val Thr Lys Gly Ala Ala Gln Ala Ser Ala Gly Pro Met
 145 150 155

gct ttg att ggc gcg att aaa atg gag act aaa agt gct agc gat ttt 651
 Ala Leu Ile Gly Ala Ile Lys Met Glu Thr Lys Ser Ala Ser Asp Phe
 160 165 170

 atc cct aaa ggt aaa gac tac gcc ata agt ggg gct gcc act ttt tta 699
 Ile Pro Lys Gly Lys Asp Tyr Ala Ile Ser Gly Ala Ala Thr Phe Leu
 175 180 185

 acc aac ttt ggg gat cga gaa acc gtg atg ggc gct tat cgt cat aat 747
 Thr Asn Phe Gly Asp Arg Glu Thr Val Met Gly Ala Tyr Arg His Asn
 190 195 200 205

 cat ttt gat gcg ctt ttg tat tac acg cat caa aat att ttt tac tat 795
 His Phe Asp Ala Leu Leu Tyr Tyr Thr His Gln Asn Ile Phe Tyr Tyr
 210 215 220

 cgt gat ggg gat aat gct aca aaa gat ctc ttt aga cct aaa gcg gag 843
 Arg Asp Gly Asp Asn Ala Thr Lys Asp Leu Phe Arg Pro Lys Ala Glu
 225 230 235

 aat aaa gtt aca gaa gtc cta gcg agc aaa aca atg tgatggctaa 889
 Asn Lys Val Thr Glu Val Leu Ala Ser Lys Thr Met
 240 245

 gatcaatggg tatttgagcg aaagggatat tttaacgctc agttataaca tgaccagaga 949
 caacgctaac 959

<210> 20
 <211> 249
 <212> PRT
 <213> Helicobacter pylori

<400> 20
 Met Asn Asp Lys Arg Phe Arg Lys Tyr Cys Ser Phe Ser Ile Phe Leu
 1 5 10 15
 Ser Leu Leu Gly Thr Phe Glu Leu Glu Ala Lys Glu Glu Glu Glu Lys
 20 25 30
 Glu Glu Arg Lys Thr Glu Arg Lys Lys Glu Lys Asn Ala Gln His Thr
 35 40 45
 Leu Gly Lys Val Thr Thr Gln Ala Ala Lys Ile Phe Asn Tyr Asn Asn
 50 55 60
 Gln Thr Thr Ile Ser Ser Lys Glu Leu Glu Arg Arg Gln Ala Asn Gln
 65 70 75 80
 Ile Ser Asp Met Phe Arg Arg Asn Pro Asn Ile Asn Val Gly Gly Gly
 85 90 95
 Ala Val Ile Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu Asp Arg Leu
 100 105 110
 Ala Arg Val Thr Val Asp Gly Ala Ala Gln Met Gly Ala Ser Tyr Gly
 115 120 125
 His Gln Gly Asn Thr Ile Ile Asp Pro Gly Met Leu Lys Ser Val Val
 130 135 140
 Val Thr Lys Gly Ala Ala Gln Ala Ser Ala Gly Pro Met Ala Leu Ile
 145 150 155 160
 Gly Ala Ile Lys Met Glu Thr Lys Ser Ala Ser Asp Phe Ile Pro Lys
 165 170 175
 Gly Lys Asp Tyr Ala Ile Ser Gly Ala Ala Thr Phe Leu Thr Asn Phe
 180 185 190
 Gly Asp Arg Glu Thr Val Met Gly Ala Tyr Arg His Asn His Phe Asp
 195 200 205

Ala Leu Leu Tyr Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly
 210 215 220
 Asp Asn Ala Thr Lys Asp Leu Phe Arg Pro Lys Ala Glu Asn Lys Val
 225 230 235 240
 Thr Glu Val Leu Ala Ser Lys Thr Met
 245

<210> 21
 <211> 1397
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (138)...(1244)

<400> 21
 tgaatgcggg cattgggggct aggtttgggc ttgattataa agatattaat atcacccggaa 60
 atattggtat gcgctatgct ttttaatggt atcattaaac ctatttttaa caatcccaat 120
 tcatagcagg atcaccc atg caa ttt caa aaa gcc tta tta cat tca tca 170
 Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser
 1 5 10
 ttc ttt tta cct tta ttt tta tct ttt tgt atc gct gaa gaa aat ggg 218
 Phe Phe Leu Pro Leu Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly
 15 20 25
 gcg tat gcg agc gtg ggt ttt gaa tat tcc att agt cat gcc gtt gaa 266
 Ala Tyr Ala Ser Val Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu
 30 35 40
 cac aat aac ccc ttt tta aat caa gaa cgc atc caa atc att tct aac 314
 His Asn Asn Pro Phe Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn
 45 50 55
 gct caa aat aaa atc tat aaa ctc cat caa gtt aaa aat gaa atc aca 362
 Ala Gln Asn Lys Ile Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr
 60 65 70 75
 agc atg cct aaa acc ttt gca tat atc aac aac gct tta aaa aac aac 410
 Ser Met Pro Lys Thr Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn
 80 85 90
 tcc aaa tta acc ccc act gaa atg caa gcc gaa caa tac tac ctc caa 458
 Ser Lys Leu Thr Pro Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln
 95 100 105
 tcc acc ttt caa aac att gaa aaa ata gta atg ctt agc ggt ggc gtt 506
 Ser Thr Phe Gln Asn Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val
 110 115 120
 tca tct aac cca caa tta gtc caa gcg ttg gaa aaa atg caa gaa ccc 554
 Ser Ser Asn Pro Gln Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro
 125 130 135
 att act aac cct tta gaa ttt gaa gaa aac tta aga aat tta gaa gtg 602
 Ile Thr Asn Pro Leu Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val
 140 145 150 155

caa ttt gct caa tct caa aac cgc atg ctt tct tct tta tct tct caa	650
Gln Phe Ala Gln Ser Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln	
160 165 170	
atc gct gcc att tca aat tcc tta aac gcg ctt gat cct aac tct tat	698
Ile Ala Ala Ile Ser Asn Ser Leu Asn Ala Leu Asp Pro Asn Ser Tyr	
175 180 185	
tct aaa aac att tca agc atg tat ggg gtg agt ttg agc gta ggt tat	746
Ser Lys Asn Ile Ser Ser Met Tyr Gly Val Ser Leu Ser Val Gly Tyr	
190 195 200	
aag cat ttc ttt acc aag aaa aaa aat caa ggg ttg cgc tat tac ttg	794
Lys His Phe Phe Thr Lys Lys Lys Asn Gln Gly Leu Arg Tyr Tyr Leu	
205 210 215	
ttt tat gac tat ggt tac act aat ttt ggt ttt gtg ggc aat ggc ttt	842
Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe	
220 225 230 235	
gat ggt tta ggc aaa atg aat aac cat ctc tat ggg ctt ggg ata gac	890
Asp Gly Leu Gly Lys Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp	
240 245 250	
tat ctt tat aat ttc att gat aat gca aaa aaa cac tct agc gta ggt	938
Tyr Leu Tyr Asn Phe Ile Asp Asn Ala Lys Lys His Ser Ser Val Gly	
255 260 265	
ttt tat ctg ggt ttt gct tta gcg ggg agt tcg tgg gta ggg agt ggt	986
Phe Tyr Leu Gly Phe Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly	
270 275 280	
ttg agc atg tgg gtg agc caa acg gat ttt atc aac aat tac ttg acg	1034
Leu Ser Met Trp Val Ser Gln Thr Asp Phe Ile Asn Asn Tyr Leu Thr	
285 290 295	
ggc tat caa gct aaa atg cac acg agt ttt ttc cag atc cct ttg aat	1082
Gly Tyr Gln Ala Lys Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn	
300 305 310 315	
ttt ggg gtt cgt gtg aat gtc aat agg cat aat ggc ttt gaa atg ggc	1130
Phe Gly Val Arg Val Asn Val Asn Arg His Asn Gly Phe Glu Met Gly	
320 325 330	
ttg aaa atc cct tta gcg atg aat tcc ttt tat gaa acg cat ggc aaa	1178
Leu Lys Ile Pro Leu Ala Met Asn Ser Phe Tyr Glu Thr His Gly Lys	
335 340 345	
ggg cta aac act tcc ctc ttt ttc aaa cgc ctt gtc atg ttt aac gtg	1226
Gly Leu Asn Thr Ser Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val	
350 355 360	
agt tac gtt tat agt ttt taggggggta gaaataagca ccccttaaa	1274
Ser Tyr Val Tyr Ser Phe	
365	
tgttatcgca acctttgaat tttaaaaact ctttagtttt tttgcctcaa atgatggacg	1334
ctctcgcccc caagaccata attattagaa tcgacctcat ctataatgac cacaatagaa	1394

gcc

1397

<210> 22
 <211> 369
 <212> PRT
 <213> Helicobacter pylori

<400> 22
 Met Gln Phe Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu
 1 5 10 15
 Phe Leu Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val
 20 25 30
 Gly Phe Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe
 35 40 45
 Leu Asn Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile
 50 55 60
 Tyr Lys Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr
 65 70 75 80
 Phe Ala Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro
 85 90 95
 Thr Glu Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn
 100 105 110
 Ile Glu Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln
 115 120 125
 Leu Val Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu
 130 135 140
 Glu Phe Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser
 145 150 155 160
 Gln Asn Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser
 165 170 175
 Asn Ser Leu Asn Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser
 180 185 190
 Ser Met Tyr Gly Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr
 195 200 205
 Lys Lys Lys Asn Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly
 210 215 220
 Tyr Thr Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys
 225 230 235 240
 Met Asn Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe
 245 250 255
 Ile Asp Asn Ala Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe
 260 265 270
 Ala Leu Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val
 275 280 285
 Ser Gln Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys
 290 295 300
 Met His Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val
 305 310 315 320
 Asn Val Asn Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu
 325 330 335
 Ala Met Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser
 340 345 350
 Leu Phe Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser
 355 360 365
 Phe

<210> 23

<211> 1030
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (342)...(824)

<400> 23
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 agccttacaa aatatcttaa ataacgctaa aagcgcgcat tttaaatttg ttttagagag 120
 ccaaaacgcc gctcaatcta ttatagaaat tcaaagcctc ttgaaacaac tctccttaaa 180
 aaataatgaa atcttttttaa tgccttttagg cacaaataac aacgagctag acaaaaatct 240
 aaaaacccta gcccccttag ccataaagca tggtttcagg ctaagcgata ggcttcatat 300
 ccgcttggtg gataatcaaa aagggtttta aaaagttaat c atg acc atc aaa gtt 356
 Met Thr Ile Lys Val
 1 5

ttt tcg ccc aaa tac ccc act gaa tta gaa gaa ttt tat gct gag cgt 404
 Phe Ser Pro Lys Tyr Pro Thr Glu Leu Glu Glu Phe Tyr Ala Glu Arg
 10 15 20

atc gct gac aac cct tta ggg ttt atc caa cgc ttg gat ctt ttg cct 452
 Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg Leu Asp Leu Leu Pro
 25 30 35

agt att agc ggg ttc gtt caa aaa ttg cgc gag cat ggc ggg gaa ttt 500
 Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu His Gly Gly Glu Phe
 40 45 50

ttt gaa atg aga gag ggt aac aag ctc att ggg att tgt ggg ctt aat 548
 Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly Ile Cys Gly Leu Asn
 55 60 65

cct atc aat caa aca gaa gcc gag ctg tgc aaa ttc cac ata aat agt 596
 Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys Phe His Ile Asn Ser
 70 75 80 85

gct tat caa tcc caa ggg cta ggt caa aaa ctc tat gag agc gtg gag 644
 Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu Tyr Glu Ser Val Glu
 90 95 100

aaa tac gct ttc att aaa ggc tat act aaa atc tct ctg cat gtg agc 692
 Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile Ser Leu His Val Ser
 105 110 115

aaa agc caa atc aag gca tgc aac ctc tat caa aag ctg ggt ttt gtg 740
 Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln Lys Leu Gly Phe Val
 120 125 130

cac atc aaa gaa gag gat tgc gtg gtg gag ttg ggc gaa gag act ttg 788
 His Ile Lys Glu Glu Asp Cys Val Val Glu Leu Gly Glu Glu Thr Leu
 135 140 145

att ttc ccc act ctt ttt atg gaa aag att ttg tct tgattggtgc 834
 Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu Ser
 150 155 160

atccatttga cacacgccca agcgacattc aaactatcaa actttcatta acacaacc 894

attaacgcta aataaacctt aaaacaaaca ctggttggtt aaattttggt tttcaagcgc 954
 ttcgcaaagt tttagaagcc ctatttaggg gttaacgcta aaataggcta tcaaaactac 1014
 tttaatgatt ttatag 1030

<210> 24
 <211> 161
 <212> PRT
 <213> Helicobacter pylori

<400> 24
 Met Thr Ile Lys Val Phe Ser Pro Lys Tyr Pro Thr Glu Leu Glu Glu
 1 5 10 15
 Phe Tyr Ala Glu Arg Ile Ala Asp Asn Pro Leu Gly Phe Ile Gln Arg
 20 25 30
 Leu Asp Leu Leu Pro Ser Ile Ser Gly Phe Val Gln Lys Leu Arg Glu
 35 40 45
 His Gly Gly Glu Phe Phe Glu Met Arg Glu Gly Asn Lys Leu Ile Gly
 50 55 60
 Ile Cys Gly Leu Asn Pro Ile Asn Gln Thr Glu Ala Glu Leu Cys Lys
 65 70 75 80
 Phe His Ile Asn Ser Ala Tyr Gln Ser Gln Gly Leu Gly Gln Lys Leu
 85 90 95
 Tyr Glu Ser Val Glu Lys Tyr Ala Phe Ile Lys Gly Tyr Thr Lys Ile
 100 105 110
 Ser Leu His Val Ser Lys Ser Gln Ile Lys Ala Cys Asn Leu Tyr Gln
 115 120 125
 Lys Leu Gly Phe Val His Ile Lys Glu Glu Asp Cys Val Val Glu Leu
 130 135 140
 Gly Glu Glu Thr Leu Ile Phe Pro Thr Leu Phe Met Glu Lys Ile Leu
 145 150 155 160
 Ser

<210> 25
 <211> 1477
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (374)...(1267)

<400> 25
 cgtggagttt tttaggcatt tctttatatt cattcaataa cgcttgcgcg ggcaattctt 60
 caactaaaat ctctactaac aattcatctg aatgcaaaat ctcaattctc cctaaaaaac 120
 aaaatcactt ttaagactaa atcatgttag aattatactt gaattttacac tcagtttagt 180
 ttattttctta atacaaaagg taggcgtttt gaaacattta accccactca ctcacaccat 240
 ctttaaagcc ttatggctag gcacagcctt aagtgcattt ttaagtttag cgcgaacaga 300
 aagccccact aaaacagagc ctaagcccgc taaaggggtt aaaaacaagc ccaaatcgcc 360
 cgttactaaa gtc atg atg acc aat tgc gac aat att aaa gat ttt aac 409
 Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn
 1 5 10
 gct aag caa aaa gaa gtc tta aaa gcc gct tat caa ttc ggc tct aaa 457
 Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys
 15 20 25
 gaa aat tta ggc tat gaa atg gca ggc att gca tgg aaa gag tca tgc 505

Glu	Asn	Leu	Gly	Tyr	Glu	Met	Ala	Gly	Ile	Ala	Trp	Lys	Glu	Ser	Cys		
30						35					40						
gca	ggg	gtt	tat	aaa	atc	aat	ttt	tcg	gat	ccg	agc	gcg	ggc	gtg	tat	553	
Ala	Gly	Val	Tyr	Lys	Ile	Asn	Phe	Ser	Asp	Pro	Ser	Ala	Gly	Val	Tyr	60	
45					50					55							
cat	tct	tat	atc	cca	agc	gtt	cta	aaa	agc	tat	ggg	cat	aat	gat	agc	601	
His	Ser	Tyr	Ile	Pro	Ser	Val	Leu	Lys	Ser	Tyr	Gly	His	Asn	Asp	Ser	75	
				65					70								
ccc	ttt	ttg	cgt	aat	gtg	atg	ggg	gaa	ttg	ctc	att	aaa	gac	gat	gcg	649	
Pro	Phe	Leu	Arg	Asn	Val	Met	Gly	Glu	Leu	Leu	Ile	Lys	Asp	Asp	Ala		
			80					85					90				
ttt	gct	tct	gaa	gtg	gct	tta	aaa	gag	ttg	ctc	tat	tgg	aaa	aca	cgc	697	
Phe	Ala	Ser	Glu	Val	Ala	Leu	Lys	Glu	Leu	Leu	Tyr	Trp	Lys	Thr	Arg		
		95					100					105					
tac	cat	gac	aat	tta	aaa	gac	atg	att	aaa	tct	tac	aac	aag	ggc	agt	745	
Tyr	His	Asp	Asn	Leu	Lys	Asp	Met	Ile	Lys	Ser	Tyr	Asn	Lys	Gly	Ser		
110						115					120						
cgt	tgg	gaa	agg	agc	gaa	aaa	tct	aac	gct	gat	gct	gaa	aaa	tat	tac	793	
Arg	Trp	Glu	Arg	Ser	Glu	Lys	Ser	Asn	Ala	Asp	Ala	Glu	Lys	Tyr	Tyr		
125					130				135						140		
gaa	gag	ata	caa	gac	aga	atc	agg	cgt	ttg	aaa	gaa	tct	aaa	atc	ttt	841	
Glu	Glu	Ile	Gln	Asp	Arg	Ile	Arg	Arg	Leu	Lys	Glu	Ser	Lys	Ile	Phe		
				145					150					155			
gat	tcg	cag	tct	agt	aat	gac	caa	gaa	ttg	caa	aaa	agc	gct	aat	agc	889	
Asp	Ser	Gln	Ser	Ser	Asn	Asp	Gln	Glu	Leu	Gln	Lys	Ser	Ala	Asn	Ser		
			160					165					170				
aac	ctg	gat	tta	gac	cct	atc	ggc	aac	gcc	atg	ccc	caa	gcc	tta	att	937	
Asn	Leu	Asp	Leu	Asp	Pro	Ile	Gly	Asn	Ala	Met	Pro	Gln	Ala	Leu	Ile		
		175					180					185					
gcc	aaa	gaa	act	aaa	ata	gaa	gaa	acc	caa	gca	gaa	aaa	tcc	caa	gaa	985	
Ala	Lys	Glu	Thr	Lys	Ile	Glu	Glu	Thr	Gln	Ala	Glu	Lys	Ser	Gln	Glu		
190						195					200						
atg	aaa	gag	aca	act	agc	gag	caa	aca	aaa	agt	aag	cca	gaa	aaa	gca	1033	
Met	Lys	Glu	Thr	Thr	Ser	Glu	Gln	Thr	Lys	Ser	Lys	Pro	Glu	Lys	Ala		
205					210					215					220		
aaa	gat	aaa	ccc	atg	tat	ttg	gcg	caa	atc	aac	agc	act	gat	ttc	aca	1081	
Lys	Asp	Lys	Pro	Met	Tyr	Leu	Ala	Gln	Ile	Asn	Ser	Thr	Asp	Phe	Thr		
				225					230					235			
ccc	gtt	aaa	aaa	agc	ccc	aaa	aaa	ccg	gct	aaa	gtg	agc	caa	aaa	cac	1129	
Pro	Val	Lys	Lys	Ser	Pro	Lys	Lys	Pro	Ala	Lys	Val	Ser	Gln	Lys	His		
			240					245					250				
tcc	ttt	aag	aat	aac	att	aaa	aat	aat	gta	aaa	aac	aac	gcc	aaa	acc	1177	
Ser	Phe	Lys	Asn	Asn	Ile	Lys	Asn	Asn	Val	Lys	Asn	Asn	Ala	Lys	Thr		
		255					260					265					

gct tcc aaa aaa caa gaa atg tgc aaa aat tgc tct cca ggg caa agg 1225
 Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro Gly Gln Arg
 270 275 280

aat gcg att tta gct aac cac atc act ctc atg caa gag ctt 1267
 Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu Leu
 285 290 295

taaaaagtcc taaaaatggc gcaaaaaact cttttgatta tcaactgatgg cattgggtat 1327
 cgtaaagata gcgatacataa cgctttcttc catgccaaaa aaccactta tgatttgatg 1387
 tttaaaacct tgccttatag cctgattgat acgcatggct tgagcgtggg cttacctaag 1447
 gggcaaatgg gaaattctga agtggggcat 1477

<210> 26
 <211> 298
 <212> PRT
 <213> Helicobacter pylori

<400> 26
 Met Met Thr Asn Cys Asp Asn Ile Lys Asp Phe Asn Ala Lys Gln Lys
 1 5 10 15
 Glu Val Leu Lys Ala Ala Tyr Gln Phe Gly Ser Lys Glu Asn Leu Gly
 20 25 30
 Tyr Glu Met Ala Gly Ile Ala Trp Lys Glu Ser Cys Ala Gly Val Tyr
 35 40 45
 Lys Ile Asn Phe Ser Asp Pro Ser Ala Gly Val Tyr His Ser Tyr Ile
 50 55 60
 Pro Ser Val Leu Lys Ser Tyr Gly His Asn Asp Ser Pro Phe Leu Arg
 65 70 75 80
 Asn Val Met Gly Glu Leu Leu Ile Lys Asp Asp Ala Phe Ala Ser Glu
 85 90 95
 Val Ala Leu Lys Glu Leu Leu Tyr Trp Lys Thr Arg Tyr His Asp Asn
 100 105 110
 Leu Lys Asp Met Ile Lys Ser Tyr Asn Lys Gly Ser Arg Trp Glu Arg
 115 120 125
 Ser Glu Lys Ser Asn Ala Asp Ala Glu Lys Tyr Tyr Glu Glu Ile Gln
 130 135 140
 Asp Arg Ile Arg Arg Leu Lys Glu Ser Lys Ile Phe Asp Ser Gln Ser
 145 150 155 160
 Ser Asn Asp Gln Glu Leu Gln Lys Ser Ala Asn Ser Asn Leu Asp Leu
 165 170 175
 Asp Pro Ile Gly Asn Ala Met Pro Gln Ala Leu Ile Ala Lys Glu Thr
 180 185 190
 Lys Ile Glu Glu Thr Gln Ala Glu Lys Ser Gln Glu Met Lys Glu Thr
 195 200 205
 Thr Ser Glu Gln Thr Lys Ser Lys Pro Glu Lys Ala Lys Asp Lys Pro
 210 215 220
 Met Tyr Leu Ala Gln Ile Asn Ser Thr Asp Phe Thr Pro Val Lys Lys
 225 230 235 240
 Ser Pro Lys Lys Pro Ala Lys Val Ser Gln Lys His Ser Phe Lys Asn
 245 250 255
 Asn Ile Lys Asn Asn Val Lys Asn Asn Ala Lys Thr Ala Ser Lys Lys
 260 265 270
 Gln Glu Met Cys Lys Asn Cys Ser Pro Gly Gln Arg Asn Ala Ile Leu
 275 280 285
 Ala Asn His Ile Thr Leu Met Gln Glu Leu
 290 295

<210> 27
 <211> 1515
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (141)...(1340)

<400> 27

ttagtgttga tttttttatc gttagtgttt gtgcgtcctt tagaggcttt gagcgtgttt 60
 atggggttgt atttgattta tggcatcatt cgggtggctct ttttaatggt aaaaattatt 120
 ttttaataaaa ataaaagcgc atg aaa gaa tct ttt tac ata gag gga atg act 173

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr
 1 5 10

tgc acg gcg tgt tct agc ggg att gaa cgc tct ttg ggg cgt aag agt 221
 Cys Thr Ala Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser
 15 20 25

ttt gtg aaa aaa ata gaa gtg agc ctt tta aat aag agc gct aac att 269
 Phe Val Lys Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile
 30 35 40

gaa ttt gac gaa aac caa acc aat tta gac gaa att ttt aaa ctc att 317
 Glu Phe Asp Glu Asn Gln Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile
 45 50 55

gaa aag cta ggc tat agc cct aaa aaa gct ctg aca aaa gaa aaa aaa 365
 Glu Lys Leu Gly Tyr Ser Pro Lys Lys Ala Leu Thr Lys Glu Lys Lys
 60 65 70 75

gaa ttt ttt agc cct aat gtt aaa tta gcg tta gcg gtt att ttc acg 413
 Glu Phe Phe Ser Pro Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr
 80 85 90

ctt ttt gtg gtg tat ctt tct atg ggg gcg atg ctt agc cct agc ctt 461
 Leu Phe Val Val Tyr Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu
 95 100 105

tta cct gaa agc ttg ctt gca att gat aat cat agt aat ttt tta aac 509
 Leu Pro Glu Ser Leu Leu Ala Ile Asp Asn His Ser Asn Phe Leu Asn
 110 115 120

gct tgc tta cag ctt ata ggc gca ctc att gtc atg cat ttg ggg agg 557
 Ala Cys Leu Gln Leu Ile Gly Ala Leu Ile Val Met His Leu Gly Arg
 125 130 135

gat ttt tac att caa ggg ttt aaa gcc tta tgg cac aga caa ccc aac 605
 Asp Phe Tyr Ile Gln Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn
 140 145 150 155

atg agc agc ctt atc gcc ata ggc aca agc gct gcc tta att tca agc 653
 Met Ser Ser Leu Ile Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ser
 160 165 170

ctg tgg caa ttg tat ttg gtc tat acc aat cat tat acc gat cag tgg 701
 Leu Trp Gln Leu Tyr Leu Val Tyr Thr Asn His Tyr Thr Asp Gln Trp
 175 180 185

tct tat ggg cat tat tat ttt gaa agc gtg tgc gtg att tta atg ttt	749
Ser Tyr Gly His Tyr Tyr Phe Glu Ser Val Cys Val Ile Leu Met Phe	
190 195 200	
gtg atg gtg ggc aaa cgc att gaa aat gtt tct aaa gac aaa gct tta	797
Val Met Val Gly Lys Arg Ile Glu Asn Val Ser Lys Asp Lys Ala Leu	
205 210 215	
gac gct atg caa gcc ttg atg aaa aac gcc cca aaa acc gcc ctt aaa	845
Asp Ala Met Gln Ala Leu Met Lys Asn Ala Pro Lys Thr Ala Leu Lys	
220 225 230 235	
atg caa aat aac caa cag att gaa gtt tta gtg gat agc att gtg gtg	893
Met Gln Asn Asn Gln Gln Ile Glu Val Leu Val Asp Ser Ile Val Val	
240 245 250	
ggg gat att cta aaa gtc ctc cct gga agc gcg att gcg gtg gat ggt	941
Gly Asp Ile Leu Lys Val Leu Pro Gly Ser Ala Ile Ala Val Asp Gly	
255 260 265	
gaa atc ata gag ggc gaa ggg gaa tta gat gag agc atg ttg agc ggc	989
Glu Ile Ile Glu Gly Glu Gly Glu Leu Asp Glu Ser Met Leu Ser Gly	
270 275 280	
gaa gcg ttg ccg gtt tat aaa aaa gtc ggc gat aaa gtc ttt tca ggg	1037
Glu Ala Leu Pro Val Tyr Lys Lys Val Gly Asp Lys Val Phe Ser Gly	
285 290 295	
aca ttc aat agc cac acg agt ttt tta atg aaa gcc acg caa aac aac	1085
Thr Phe Asn Ser His Thr Ser Phe Leu Met Lys Ala Thr Gln Asn Asn	
300 305 310 315	
aaa aac agc acc ttg tct caa att ata gaa atg att tat aac gct caa	1133
Lys Asn Ser Thr Leu Ser Gln Ile Ile Glu Met Ile Tyr Asn Ala Gln	
320 325 330	
agt tca aag gca gag att tct cgc tta gcg gat aag gtt tca agc gtg	1181
Ser Ser Lys Ala Glu Ile Ser Arg Leu Ala Asp Lys Val Ser Ser Val	
335 340 345	
ttt gtg cca agc gtg atc gct att tct att tta gcg ttt gtg gtg tgg	1229
Phe Val Pro Ser Val Ile Ala Ile Ser Ile Leu Ala Phe Val Val Trp	
350 355 360	
ctc atc att gca cct aag ccc gat ttt tgg tgg aat ttt gga atc gct	1277
Leu Ile Ile Ala Pro Lys Pro Asp Phe Trp Trp Asn Phe Gly Ile Ala	
365 370 375	
tta gaa gtg ttt gta tgc gtt tta gtg att tct tgc cct tgc gct tta	1325
Leu Glu Val Phe Val Ser Val Leu Val Ile Ser Cys Pro Cys Ala Leu	
380 385 390 395	
gga ttg cta cgc cta tgagcatttt agtagcgaac cagaaagcga gttctttagg	1380
Gly Leu Leu Arg Leu	
400	
gttatttttt aaagacgcta aaagttaga aaaagcaagg ctagtcaata cgatcgTTTT	1440
tgataaaacc ggcacgctca ctaacggcaa gcctgtcgTTT aaaagcgTTC attctaagat	1500

agaattatta gagtt

1515

<210> 28

<211> 400

<212> PRT

<213> Helicobacter pylori

<400> 28

Met	Lys	Glu	Ser	Phe	Tyr	Ile	Glu	Gly	Met	Thr	Cys	Thr	Ala	Cys	Ser	
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Ser	Gly	Ile	Glu	Arg	Ser	Leu	Gly	Arg	Lys	Ser	Phe	Val	Lys	Lys	Ile	
			20					25					30			
Glu	Val	Ser	Leu	Leu	Asn	Lys	Ser	Ala	Asn	Ile	Glu	Phe	Asp	Glu	Asn	
			35					40				45				
Gln	Thr	Asn	Leu	Asp	Glu	Ile	Phe	Lys	Leu	Ile	Glu	Lys	Leu	Gly	Tyr	
	50					55					60					
Ser	Pro	Lys	Lys	Ala	Leu	Thr	Lys	Glu	Lys	Lys	Glu	Phe	Phe	Ser	Pro	
65					70				75						80	
Asn	Val	Lys	Leu	Ala	Leu	Ala	Val	Ile	Phe	Thr	Leu	Phe	Val	Val	Tyr	
				85					90					95		
Leu	Ser	Met	Gly	Ala	Met	Leu	Ser	Pro	Ser	Leu	Leu	Pro	Glu	Ser	Leu	
			100					105					110			
Leu	Ala	Ile	Asp	Asn	His	Ser	Asn	Phe	Leu	Asn	Ala	Cys	Leu	Gln	Leu	
		115					120					125				
Ile	Gly	Ala	Leu	Ile	Val	Met	His	Leu	Gly	Arg	Asp	Phe	Tyr	Ile	Gln	
	130					135					140					
Gly	Phe	Lys	Ala	Leu	Trp	His	Arg	Gln	Pro	Asn	Met	Ser	Ser	Leu	Ile	
145					150					155					160	
Ala	Ile	Gly	Thr	Ser	Ala	Ala	Leu	Ile	Ser	Ser	Leu	Trp	Gln	Leu	Tyr	
				165					170					175		
Leu	Val	Tyr	Thr	Asn	His	Tyr	Thr	Asp	Gln	Trp	Ser	Tyr	Gly	His	Tyr	
			180					185					190			
Tyr	Phe	Glu	Ser	Val	Cys	Val	Ile	Leu	Met	Phe	Val	Met	Val	Gly	Lys	
		195					200					205				
Arg	Ile	Glu	Asn	Val	Ser	Lys	Asp	Lys	Ala	Leu	Asp	Ala	Met	Gln	Ala	
	210					215					220					
Leu	Met	Lys	Asn	Ala	Pro	Lys	Thr	Ala	Leu	Lys	Met	Gln	Asn	Asn	Gln	
225					230					235					240	
Gln	Ile	Glu	Val	Leu	Val	Asp	Ser	Ile	Val	Val	Gly	Asp	Ile	Leu	Lys	
			245						250					255		
Val	Leu	Pro	Gly	Ser	Ala	Ile	Ala	Val	Asp	Gly	Glu	Ile	Ile	Glu	Gly	
		260						265					270			
Glu	Gly	Glu	Leu	Asp	Glu	Ser	Met	Leu	Ser	Gly	Glu	Ala	Leu	Pro	Val	
		275					280					285				
Tyr	Lys	Lys	Val	Gly	Asp	Lys	Val	Phe	Ser	Gly	Thr	Phe	Asn	Ser	His	
	290					295					300					
Thr	Ser	Phe	Leu	Met	Lys	Ala	Thr	Gln	Asn	Asn	Lys	Asn	Ser	Thr	Leu	
305					310					315					320	
Ser	Gln	Ile	Ile	Glu	Met	Ile	Tyr	Asn	Ala	Gln	Ser	Ser	Lys	Ala	Glu	
			325						330					335		
Ile	Ser	Arg	Leu	Ala	Asp	Lys	Val	Ser	Ser	Val	Phe	Val	Pro	Ser	Val	
			340					345					350			
Ile	Ala	Ile	Ser	Ile	Leu	Ala	Phe	Val	Val	Trp	Leu	Ile	Ile	Ala	Pro	
		355					360					365				
Lys	Pro	Asp	Phe	Trp	Trp	Asn	Phe	Gly	Ile	Ala	Leu	Glu	Val	Phe	Val	
	370					375					380					
Ser	Val	Leu	Val	Ile	Ser	Cys	Pro	Cys	Ala	Leu	Gly	Leu	Leu	Arg	Leu	
385					390					395					400	

<210> 29
 <211> 1443
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (76)...(1389)

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 tagtagagag atggg atg aaa aaa ata tgg ctt tta gtg tgg ggc ttg tgt 111
 Met Lys Lys Ile Trp Leu Leu Val Trp Gly Leu Cys
 1 5 10

tct tgg gtg ttt ttg cat gcg ata gag atg ata gaa aaa gcc cct aca 159
 Ser Trp Val Phe Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr
 15 20 25

aat gta gag gat aga gac aaa gcc ccc cat ttg ttg ctt tta gca ggg 207
 Asn Val Glu Asp Arg Asp Lys Ala Pro His Leu Leu Leu Leu Ala Gly
 30 35 40

att caa ggc gat gag cct ggt ggg ttt aat gca act aat ttg ttt tta 255
 Ile Gln Gly Asp Glu Pro Gly Gly Phe Asn Ala Thr Asn Leu Phe Leu
 45 50 55 60

atg cat tat agc gtt tta aaa ggt ttg gtt gaa gtg gtt cct gta ttg 303
 Met His Tyr Ser Val Leu Lys Gly Leu Val Glu Val Val Pro Val Leu
 65 70 75

aat aag cct tcc atg tta aga aat cat agg ggc ttg tat ggg gat atg 351
 Asn Lys Pro Ser Met Leu Arg Asn His Arg Gly Leu Tyr Gly Asp Met
 80 85 90

aac cgc aaa ttt gcc gct tta gac aag aat gac cct gaa tac ccc act 399
 Asn Arg Lys Phe Ala Ala Leu Asp Lys Asn Asp Pro Glu Tyr Pro Thr
 95 100 105

atc cag gaa atc aaa tcc ttg att gca aaa ccc agt ata gac gct gtc 447
 Ile Gln Glu Ile Lys Ser Leu Ile Ala Lys Pro Ser Ile Asp Ala Val
 110 115 120

ttg cat ttg cat gat ggc ggt ggg tat tac cgc cct gtt tat gtt gat 495
 Leu His Leu His Asp Gly Gly Gly Tyr Tyr Arg Pro Val Tyr Val Asp
 125 130 135 140

gcg atg ctc aat cct aag cgc tgg ggg aat tgc ttt att att gat caa 543
 Ala Met Leu Asn Pro Lys Arg Trp Gly Asn Cys Phe Ile Ile Asp Gln
 145 150 155

gat gag gtt aaa ggg gcg aaa ttc cct aat ttg ctt gct ttt gca aac 591
 Asp Glu Val Lys Gly Ala Lys Phe Pro Asn Leu Leu Ala Phe Ala Asn
 160 165 170

aat acg att gag agt atc aac gcc cat tta ttg cac ccc att gaa gag 639
 Asn Thr Ile Glu Ser Ile Asn Ala His Leu Leu His Pro Ile Glu Glu
 175 180 185

tat cat tta aaa aac acg cgc acc gcg caa ggc gat aca gaa atg caa	687
Tyr His Leu Lys Asn Thr Arg Thr Ala Gln Gly Asp Thr Glu Met Gln	
190 195 200	
aaa gcc cta act ttt tat gcg atc aac caa aaa aag agc gct ttt gcc	735
Lys Ala Leu Thr Phe Tyr Ala Ile Asn Gln Lys Lys Ser Ala Phe Ala	
205 210 215 220	
aat gaa gct agc aaa gaa ctc cct tta gca tca agg gtg ttt tac cac	783
Asn Glu Ala Ser Lys Glu Leu Pro Leu Ala Ser Arg Val Phe Tyr His	
225 230 235	
ctg caa gcc att gag ggc tta ctc aat cag ctc aat atc cct ttt aag	831
Leu Gln Ala Ile Glu Gly Leu Leu Asn Gln Leu Asn Ile Pro Phe Lys	
240 245 250	
cgc gat ttt gat ctt aac cct aac agc gtg cat gcc cta atc aat gat	879
Arg Asp Phe Asp Leu Asn Pro Asn Ser Val His Ala Leu Ile Asn Asp	
255 260 265	
aaa aac ttg tgg gca aaa atc agc tct ttg cct aaa atg ccc ctt ttt	927
Lys Asn Leu Trp Ala Lys Ile Ser Ser Leu Pro Lys Met Pro Leu Phe	
270 275 280	
aac ttg cgc cct aaa ctc aat cat ttc ccc tta ccc cac aac act aaa	975
Asn Leu Arg Pro Lys Leu Asn His Phe Pro Leu Pro His Asn Thr Lys	
285 290 295 300	
atc cca caa atc ccc ata gag agc aac gct tac att gta ggg cta gtc	1023
Ile Pro Gln Ile Pro Ile Glu Ser Asn Ala Tyr Ile Val Gly Leu Val	
305 310 315	
aaa aat aaa caa gaa gtg ttt tta aaa tac gcg aac aag ctc atg aca	1071
Lys Asn Lys Gln Glu Val Phe Leu Lys Tyr Gly Asn Lys Leu Met Thr	
320 325 330	
cga tta tcg cct ttt tac ata gag ttt gat cct tct tta gaa gaa gtg	1119
Arg Leu Ser Pro Phe Tyr Ile Glu Phe Asp Pro Ser Leu Glu Glu Val	
335 340 345	
aaa atg caa att gac aat aag gat caa atg gtt aaa ata ggg agc gtg	1167
Lys Met Gln Ile Asp Asn Lys Asp Gln Met Val Lys Ile Gly Ser Val	
350 355 360	
gtt gaa gtg aaa gag agt ttt tat atc cat gct atg gac aat atc cgt	1215
Val Glu Val Lys Glu Ser Phe Tyr Ile His Ala Met Asp Asn Ile Arg	
365 370 375 380	
gcg aat gtg att ggc ttt agc gtt tct aat gaa aat aag cct aat gaa	1263
Ala Asn Val Ile Gly Phe Ser Val Ser Asn Glu Asn Lys Pro Asn Glu	
385 390 395	
gcg ggt tat acg att aaa ttt aaa gat ttt caa aaa cgc ttt tca ttg	1311
Ala Gly Tyr Thr Ile Lys Phe Lys Asp Phe Gln Lys Arg Phe Ser Leu	
400 405 410	
gac aag caa gaa agg atc tat cgc ata gaa ttt tat aaa aac aac gcg	1359
Asp Lys Gln Glu Arg Ile Tyr Arg Ile Glu Phe Tyr Lys Asn Asn Ala	
415 420 425	

ttt agc ggg atg atc tta gtg aaa ttt gtg taggaatgga taaatctcat 1409
Phe Ser Gly Met Ile Leu Val Lys Phe Val
430 435

tgccttttaa cattcaagg ttttggatt tttt 1443

<210> 30
<211> 438
<212> PRT
<213> Helicobacter pylori

<400> 30
Met Lys Lys Ile Trp Leu Leu Val Trp Gly Leu Cys Ser Trp Val Phe
1 5 10 15
Leu His Ala Ile Glu Met Ile Glu Lys Ala Pro Thr Asn Val Glu Asp
20 25 30
Arg Asp Lys Ala Pro His Leu Leu Leu Leu Ala Gly Ile Gln Gly Asp
35 40 45
Glu Pro Gly Gly Phe Asn Ala Thr Asn Leu Phe Leu Met His Tyr Ser
50 55 60
Val Leu Lys Gly Leu Val Glu Val Val Pro Val Leu Asn Lys Pro Ser
65 70 75 80
Met Leu Arg Asn His Arg Gly Leu Tyr Gly Asp Met Asn Arg Lys Phe
85 90 95
Ala Ala Leu Asp Lys Asn Asp Pro Glu Tyr Pro Thr Ile Gln Glu Ile
100 105 110
Lys Ser Leu Ile Ala Lys Pro Ser Ile Asp Ala Val Leu His Leu His
115 120 125
Asp Gly Gly Gly Tyr Tyr Arg Pro Val Tyr Val Asp Ala Met Leu Asn
130 135 140
Pro Lys Arg Trp Gly Asn Cys Phe Ile Ile Asp Gln Asp Glu Val Lys
145 150 155 160
Gly Ala Lys Phe Pro Asn Leu Leu Ala Phe Ala Asn Asn Thr Ile Glu
165 170 175
Ser Ile Asn Ala His Leu Leu His Pro Ile Glu Glu Tyr His Leu Lys
180 185 190
Asn Thr Arg Thr Ala Gln Gly Asp Thr Glu Met Gln Lys Ala Leu Thr
195 200 205
Phe Tyr Ala Ile Asn Gln Lys Lys Ser Ala Phe Ala Asn Glu Ala Ser
210 215 220
Lys Glu Leu Pro Leu Ala Ser Arg Val Phe Tyr His Leu Gln Ala Ile
225 230 235 240
Glu Gly Leu Leu Asn Gln Leu Asn Ile Pro Phe Lys Arg Asp Phe Asp
245 250 255
Leu Asn Pro Asn Ser Val His Ala Leu Ile Asn Asp Lys Asn Leu Trp
260 265 270
Ala Lys Ile Ser Ser Leu Pro Lys Met Pro Leu Phe Asn Leu Arg Pro
275 280 285
Lys Leu Asn His Phe Pro Leu Pro His Asn Thr Lys Ile Pro Gln Ile
290 295 300
Pro Ile Glu Ser Asn Ala Tyr Ile Val Gly Leu Val Lys Asn Lys Gln
305 310 315 320
Glu Val Phe Leu Lys Tyr Gly Asn Lys Leu Met Thr Arg Leu Ser Pro
325 330 335
Phe Tyr Ile Glu Phe Asp Pro Ser Leu Glu Glu Val Lys Met Gln Ile
340 345 350
Asp Asn Lys Asp Gln Met Val Lys Ile Gly Ser Val Val Glu Val Lys
355 360 365

Glu	Ser	Phe	Tyr	Ile	His	Ala	Met	Asp	Asn	Ile	Arg	Ala	Asn	Val	Ile
370						375					380				
Gly	Phe	Ser	Val	Ser	Asn	Glu	Asn	Lys	Pro	Asn	Glu	Ala	Gly	Tyr	Thr
385					390					395					400
Ile	Lys	Phe	Lys	Asp	Phe	Gln	Lys	Arg	Phe	Ser	Leu	Asp	Lys	Gln	Glu
				405					410					415	
Arg	Ile	Tyr	Arg	Ile	Glu	Phe	Tyr	Lys	Asn	Asn	Ala	Phe	Ser	Gly	Met
			420					425					430		
Ile	Leu	Val	Lys	Phe	Val										
			435												

<210> 31
 <211> 1280
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (66)...(1223)

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 ttcaa atg tta agg aaa aac att tta gct tac tat ggg gcg aat ttt ctc 110
 Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu
 1 5 10 15

tta atc atc gct caa agc tta ccc cat gcg att tta acc ccc ttg ttg 158
 Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu
 20 25 30

ctt tct aaa ggg ctt agt ttg agt gaa atc ttg ctc gtg caa acc ttt 206
 Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe
 35 40 45

ttt agc ttt tgc gtg cta gtg gct gaa tac cca agc ggc gtt tta gcg 254
 Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala
 50 55 60

gat ttg atg agc cga aaa aat tta ttc ctg gtt tct aat gcc ttt tta 302
 Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu
 65 70 75

atc gct agt ttt tcg ttt gtg ctg ttt ttt gat agc ttt att ttc atg 350
 Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met
 80 85 90 95

ctt tta gcg tgg ggg ttg tat ggt ttg tat agc gca tgc tct agc ggc 398
 Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly
 100 105 110

acg att gaa gct tca ctc atc aca gac att aag gaa aac aaa aaa gat 446
 Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp
 115 120 125

tta tcc aag ttt tta gcc aaa aac aat caa att act tat tta ggc atg 494
 Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met
 130 135 140

att ata ggg agt tct ttg gga tcg ttt ttg tat ctc aaa gtc cat gcg Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala 145 150 155	542
atg ctg tat att gtg ggg att ttt tta atc atg ctc tgt gtg cta acg Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr 160 165 170 175	590
atc att ttt tat ttt aaa gag aaa gaa ggg gat ttt aaa agc caa aaa Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys 180 185 190	638
agc ctg aaa ctc ctt aaa gag caa gtc aaa ggc agt ctt aaa gag ctt Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu 195 200 205	686
aaa gat aac ccc aaa ctt aaa att ctg tta gtg ggg cat ttg att acg Lys Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr 210 215 220	734
ccc gtc ttt ttt atg agc cat ttt caa atg tgg caa gcg tat ttt tta Pro Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu 225 230 235	782
aaa caa ggc gtt aaa gag caa tac ctt ttt gtg ttt tat atc gct ttt Lys Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe 240 245 250 255	830
caa gtg att tct att ctc att cat ttt tta aaa gcc tct agt tat agc Gln Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser 260 265 270	878
caa aaa atc gcc ttg agt tcg ctt gtg gtg ttg tta ggc gtt agc ccc Gln Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro 275 280 285	926
tta ttg ctt agc aat atc cct tat tgt ttc ata ggg gtg tat gcg ctc Leu Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu 290 295 300	974
atg gtg gcg ttt ttc act tac atg agc tat tgc tta aac tat caa ttc Met Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe 305 310 315	1022
tcc aaa ttc gtt tct aaa aac aac att tcc tcg ctc tca tcg ctt tta Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu 320 325 330 335	1070
tca agc tgt gtg cgc gtg gtc tct gtg cta atc tta tcg ctc agc agt Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser 340 345 350	1118
ctg gaa ctg cgt tac ttc tca ccc cta act atc ata acc atg cat ttt Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe 355 360 365	1166
gcc ttg acg ctt atc atc ctc ttt ttc ttt ttg tat aag gct aag ccg Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro 370 375 380	1214

ttt gat gag tgagcggcgtt taagagtgcacaccttttagc gattttctata
Phe Asp Glu
385

1263

gcaacatcat agccatg

1280

<210> 32
<211> 386
<212> PRT
<213> Helicobacter pylori

<400> 32
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1 5 10 15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
20 25 30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
35 40 45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
50 55 60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile
65 70 75 80
Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu
85 90 95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
100 105 110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
115 120 125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
130 135 140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145 150 155 160
Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile
165 170 175
Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser
180 185 190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
195 200 205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
210 215 220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225 230 235 240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245 250 255
Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln
260 265 270
Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro Leu
275 280 285
Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met
290 295 300
Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser
305 310 315 320
Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu Ser
325 330 335
Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser Leu
340 345 350
Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe Ala
355 360 365

Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro Phe
 370 375 380
 Asp Glu
 385

<210> 33
 <211> 1264
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (51)...(1205)

<400> 33
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 Met Glu
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tca gta aaa aca gga aaa aca aat aag gtt ggc aag aat aca gag atg 104
 Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr Glu Met
 5 10 15

gct aat aca aag gca aat aaa gag gct cat ttt aaa caa gcg agc acc 152
 Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala Ser Thr
 20 25 30

att aca aat ata atc aga tca att cgt ggg att ttt aca aaa att gca 200
 Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys Ile Ala
 35 40 45 50

aag aaa gtt aga gga ctt gta aaa aaa cac ccc aag aaa agc agt gcg 248
 Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser Ser Ala
 55 60 65

gca tta gta gta ttg acc cat att gcg tgc aag aaa gcg aaa gaa tta 296
 Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys Glu Leu
 70 75 80

gac gat aaa gtc caa gat aaa tcc aaa caa gct gaa aaa gaa aat caa 344
 Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn Gln
 85 90 95

atc aat tgg tgg aaa tat tca gga tta aca ata gcg aca agt tta tta 392
 Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu Leu
 100 105 110

tta gcc gct tgt agc act ggt gat gtt agt gaa caa ata gaa cta gaa 440
 Leu Ala Ala Cys Ser Thr Gly Asp Val Ser Glu Gln Ile Glu Leu Glu
 115 120 125 130

caa gaa aaa caa aag acg agc aat ata gag act aac aat caa ata aaa 488
 Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
 135 140 145

gta gaa caa gaa aaa caa aag aca agc aat ata gag act aat aat caa 536
 Val Glu Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln
 150 155 160

ata aaa gta gaa caa gaa caa cag aaa aca gaa caa gaa mga cag aaa	584
Ile Lys Val Glu Gln Glu Gln Lys Thr Glu Gln Glu Xaa Gln Lys	
165 170 175	
aca gaa caa gaa aga cag aag aca gaa caa gaa aaa caa aag acc att	632
Thr Glu Gln Glu Arg Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Ile	
180 185 190	
aaa aca cag aaa gat ttc att aaa tat gta gaa caa aat tgc caa gaa	680
Lys Thr Gln Lys Asp Phe Ile Lys Tyr Val Glu Gln Asn Cys Gln Glu	
195 200 205 210	
aat cat aat caa ttc ttt att gaa aaa gga gga att aag gct ggt att	728
Asn His Asn Gln Phe Phe Ile Glu Lys Gly Gly Ile Lys Ala Gly Ile	
215 220 225	
ggt ata gaa gta gaa gct gaa tgc aaa acc cct aaa cct gca aaa acc	776
Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr	
230 235 240	
aat caa acc cct atc cag cca aaa cac ctc cca aac tct aaa caa ccc	824
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro	
245 250 255	
cgc tct caa aga gga tca aaa gcg caa gag ctt atc gct tat ttg caa	872
Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln	
260 265 270	
aaa gag cta gaa tct ctg ccc tat tca caa aaa gct atc gct aaa caa	920
Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln	
275 280 285 290	
gtg gat ttt tat aga cca agt tct atc gct tat tta gaa cta gac cct	968
Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro	
295 300 305	
aga gat ttt aat gtt aca gaa gaa tgg caa aaa gaa aat tta aaa ata	1016
Arg Asp Phe Asn Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile	
310 315 320	
cgc tct aaa gct caa gct aaa atg ctt gaa atg agg agt tta aaa cca	1064
Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu Lys Pro	
325 330 335	
gac tca caa gcc cac ctt tca acc tct caa agc ctt ttg ttc gtt caa	1112
Asp Ser Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Phe Val Gln	
340 345 350	
aaa ata ttt gct gat gtt aat aaa gaa ata aaa gta gtt gct aat act	1160
Lys Ile Phe Ala Asp Val Asn Lys Glu Ile Lys Val Val Ala Asn Thr	
355 360 365 370	
gaa aag aaa gca gaa aaa gcg ggt tat ggt tat agt aaa agg atg	1205
Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met	
375 380 385	
taggcataag aaaacacccat aaaatcggtc ttagcttatt tatagtattt taaaaactc	1264

<210> 34
 <211> 385
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 176
 <223> Xaa = any amino acid

<400> 34

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Glu	Met	Ala	Asn	Thr	Lys	Ala	Asn	Lys	Glu	Ala	His	Phe	Lys	Gln	Ala
			20					25					30		
Ser	Thr	Ile	Thr	Asn	Ile	Ile	Arg	Ser	Ile	Arg	Gly	Ile	Phe	Thr	Lys
		35					40					45			
Ile	Ala	Lys	Lys	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	Lys	Ser
	50					55					60				
Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	Ala	Lys
	65				70					75					80
Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu
			85					90					95		
Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser
			100					105					110		
Leu	Leu	Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	Ile	Glu
		115					120					125			
Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln
	130					135					140				
Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn
	145				150					155					160
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Glu	Gln	Glu	Xaa
			165					170					175		
Gln	Lys	Thr	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys
		180						185					190		
Thr	Ile	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys
		195				200						205			
Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala
	210				215						220				
Gly	Ile	Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala
	225				230					235					240
Lys	Thr	Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys
			245					250					255		
Gln	Pro	Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr
		260					265						270		
Leu	Gln	Lys	Glu	Leu	Glu	Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala
		275					280					285			
Lys	Gln	Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu
	290					295					300				
Asp	Pro	Arg	Asp	Phe	Asn	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu
	305				310					315					320
Lys	Ile	Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Ser	Leu
			325					330					335		
Lys	Pro	Asp	Ser	Gln	Ala	His	Leu	Ser	Thr	Ser	Gln	Ser	Leu	Leu	Phe
		340					345						350		
Val	Gln	Lys	Ile	Phe	Ala	Asp	Val	Asn	Lys	Glu	Ile	Lys	Val	Val	Ala
	355					360					365				
Asn	Thr	Glu	Lys	Lys	Ala	Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg
	370					375					380				

Met
385

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<211> 410
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (62)...(340)

<400> 35
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t atg aaa aag caa atc ttg aca ggt gtt tta tta tca gtt ttg gca gtg 109
Met Lys Lys Gln Ile Leu Thr Gly Val Leu Leu Ser Val Leu Ala Val
1 5 10 15
agt tct gca tac gct cac aaa gat aaa aaa gac gcc aaa aaa cct aaa 157
Ser Ser Ala Tyr Ala His Lys Asp Lys Lys Asp Ala Lys Lys Pro Lys
20 25 30
ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa gac gct aaa 205
Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys Asp Ala Lys
35 40 45
aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac gac aaa aaa 253
Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys
50 55 60
gac gct aaa aaa cct aaa ttt agc aca gaa tta gtc gtg gct caa aac 301
Asp Ala Lys Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn
65 70 75 80
gac aaa aaa gac gct aaa aaa cct aaa aac tca gtg gtc taatggcttt 350
Asp Lys Lys Asp Ala Lys Lys Pro Lys Asn Ser Val Val
85 90
gactctaaaa aagcggtttt aaaaacgctt ttttgatat tatectataa tttcctacca 410

<210> 36
<211> 93
<212> PRT
<213> Helicobacter pylori

<400> 36
Met Lys Lys Gln Ile Leu Thr Gly Val Leu Leu Ser Val Leu Ala Val
1 5 10 15
Ser Ser Ala Tyr Ala His Lys Asp Lys Lys Asp Ala Lys Lys Pro Lys
20 25 30
Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys Asp Ala Lys
35 40 45
Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn Asp Lys Lys
50 55 60
Asp Ala Lys Lys Pro Lys Phe Ser Thr Glu Leu Val Val Ala Gln Asn
65 70 75 80
Asp Lys Lys Asp Ala Lys Lys Pro Lys Asn Ser Val Val

<210> 37
 <211> 2097
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (67)...(2046)

<400> 37
 taaaaacccc tatcataggg cgtggcatga agaaaaaagc aaaagtcttt tggattgtt 60
 ttaatc atg att tat tgg ttg tat ttg gcg gtc ttt ttt ttg ttg agc 108
 Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser
 1 5 10

gca tta gac gct aaa gaa atc gct atg caa cga ttt gac aaa caa aac 156
 Ala Leu Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn
 15 20 25 30

cat aag att ttt gaa atc ctt gcg gat aaa gtg agc gct aaa gac aat 204
 His Lys Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn
 35 40 45

gtg ata acc gca tca ggg aat gcg atc tta ttg aat tat gat gtg tat 252
 Val Ile Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr
 50 55 60

att cta gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta 300
 Ile Leu Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu
 65 70 75

tta gag ggg aat atc aag gtt tat agg ggc gag ggt ttg ctc gtt aaa 348
 Leu Glu Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys
 80 85 90

acc gat tac gtg aaa ttg agt ttg aat gaa aaa tat gaa atc att ttc 396
 Thr Asp Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe
 95 100 105 110

ccc ttt tat gtc caa gac agc gtg agc ggg att tgg gtg agc gcg gat 444
 Pro Phe Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp
 115 120 125

att gcc agc gga aag gat caa aaa tat aag gtt aaa aac atg agc act 492
 Ile Ala Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr
 130 135 140

tca ggg tgc agc att gat aac ccc att tgg cat gtc aat gcg act tca 540
 Ser Gly Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser
 145 150 155

ggc tca ttc aac atg caa aaa tcg cat ttg tct atg tgg aat cct aag 588
 Gly Ser Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys
 160 165 170

atc tat gtc ggt gat att cct gta ttg tat ttg ccc tat att ttc atg 636

Ile 175	Tyr	Val	Gly	Asp	Ile 180	Pro	Val	Leu	Tyr	Leu 185	Pro	Tyr	Ile	Phe	Met 190	
tcc Ser	acg Thr	agc Ser	aat Asn	aaa Lys 195	aga Arg	act Thr	act Thr	ggg Gly	ttt Phe 200	tta Leu	tac Tyr	cct Pro	gag Glu	ttt Phe 205	ggc Gly	684
act Thr	tcc Ser	aac Asn	tta Leu 210	gac Asp	ggc Gly	ttt Phe	att Ile	tat Tyr 215	ttg Leu	caa Gln	ccc Pro	ttt Phe	tat Tyr 220	tta Leu	gcc Ala	732
ccc Pro	aaa Lys	aac Asn 225	tca Ser	tgg Trp	gat Asp	atg Met	acc Thr 230	ttt Phe	acc Thr	cca Pro	caa Gln	atc Ile 235	cgc Arg	tat Tyr	aaa Lys	780
agg Arg	ggt Gly 240	ttt Phe	ggc Gly	ttg Leu	aat Asn	ttt Phe 245	gaa Glu	gcg Ala	cgc Arg	tac Tyr	att Ile 250	aac Asn	tct Ser	aaa Lys	aac Asn	828
gac Asp 255	agg Arg	ttt Phe	tta Leu	ttc Phe	aac Asn 260	gcg Ala	cgc Arg	tat Tyr	ttt Phe	agg Arg 265	aat Asn	tac Tyr	acc Thr	caa Gln	tat Tyr 270	876
gtc Val	aaa Lys	cgc Arg	tac Tyr	gat Asp 275	ttg Leu	agg Arg	aat Asn	caa Gln 280	aat Asn	atc Ile	tac Tyr	ggg Gly	ttt Phe	gaa Glu 285	ttt Phe	924
tta Leu	agc Ser	tct Ser	agc Ser 290	agg Arg	gac Asp	act Thr	tta Leu 295	caa Gln	aaa Lys	tac Tyr	ttc Phe	cac His	ctt Leu 300	aag Lys	tct Ser	972
aat Asn	att Ile	gac Asp 305	aac Asn	ggg Gly	cat His	tac Tyr	att Ile 310	gac Asp	ttt Phe	tta Leu	tac Tyr	atg Met 315	aac Asn	gat Asp	ttg Leu	1020
gac Asp 320	tat Tyr	gtg Val	cgt Arg	ttt Phe	gaa Glu	aag Lys 325	ggt Val	aat Asn	aag Lys	cgt Arg	atc Ile 330	aca Thr	gac Asp	gcc Ala	acg Thr	1068
cac His 335	atg Met	tct Ser	agg Arg	gcg Ala	aat Asn 340	tac Tyr	tat Tyr	ttg Leu	caa Gln 345	aca Thr	gaa Glu	aac Asn	aat Asn	tat Tyr	tac Tyr 350	1116
ggc Gly	ttg Leu	aat Asn	atc Ile	aag Lys 355	tat Tyr	ttt Phe	tta Leu	aac Asn	ctg Leu 360	aat Asn	aaa Lys	atc Ile	aac Asn	aat Asn 365	aac Asn	1164
cgc Arg	act Thr	ttc Phe	caa Gln 370	tct Ser	gtc Val	cct Pro	aat Asn 375	ttg Leu	caa Gln	tac Tyr	cat His	aaa Lys	tat Tyr 380	tta Leu	aat Asn	1212
tct Ser	ttg Leu	tat Tyr	ttt Phe 385	aga Arg	aat Asn	ttg Leu	ttg Leu 390	tat Tyr	tcg Ser	gtg Val	gat Asp	tat Tyr 395	cag Gln	ttt Phe	aga Arg	1260
aac Asn 400	acc Thr	gca Ala	aga Arg	gag Glu	att Ile	ggt Gly 405	tat Tyr	ggc Gly	tat Tyr	gtg Val	caa Gln 410	aac Asn	gct Ala	ttg Leu	aat Asn	1308

gtg	ccg	gtg	ggc	ttg	caa	ttt	tct	ttg	ttt	aaa	aag	tat	ttg	tct	tta	1356
Val	Pro	Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	
415					420					425					430	
ggg	ctt	tgg	aat	gat	ctc	caa	cta	tct	aat	gtg	gct	tta	atg	caa	tct	1404
Gly	Leu	Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	
				435					440					445		
aaa	aat	tcc	ttc	gtg	cct	acg	atc	cct	aat	gaa	tca	agg	gaa	ttt	ggg	1452
Lys	Asn	Ser	Phe	Val	Pro	Thr	Ile	Pro	Asn	Glu	Ser	Arg	Glu	Phe	Gly	
			450					455					460			
aat	ttt	gtg	tct	tca	aat	ttt	tcc	atg	tat	gtc	aat	acg	gat	ttg	gct	1500
Asn	Phe	Val	Ser	Ser	Asn	Phe	Ser	Met	Tyr	Val	Asn	Thr	Asp	Leu	Ala	
		465					470					475				
aga	gaa	tac	aac	aag	ctt	ttc	cac	acg	atc	caa	cta	gaa	gcg	att	ttc	1548
Arg	Glu	Tyr	Asn	Lys	Leu	Phe	His	Thr	Ile	Gln	Leu	Glu	Ala	Ile	Phe	
	480					485					490					
aac	atc	cct	tat	tac	acc	ttt	aaa	aac	ggc	tta	ttt	tct	caa	aac	atg	1596
Asn	Ile	Pro	Tyr	Tyr	Thr	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	
495					500					505					510	
tat	gct	tta	agc	gcg	caa	gcc	tta	aac	agc	tac	act	tcg	cct	tta	ttg	1644
Tyr	Ala	Leu	Ser	Ala	Gln	Ala	Leu	Asn	Ser	Tyr	Thr	Ser	Pro	Leu	Leu	
				515					520					525		
aga	gat	tat	gat	tat	caa	ggg	cgt	ttg	tat	gac	tcg	gtg	tgg	aat	cct	1692
Arg	Asp	Tyr	Asp	Tyr	Gln	Gly	Arg	Leu	Tyr	Asp	Ser	Val	Trp	Asn	Pro	
			530					535					540			
agc	agt	att	tta	cct	agc	aat	gcg	agc	aac	aag	acg	gtg	gat	tta	acc	1740
Ser	Ser	Ile	Leu	Pro	Ser	Asn	Ala	Ser	Asn	Lys	Thr	Val	Asp	Leu	Thr	
		545					550					555				
cta	acg	caa	tac	ctt	tat	ggc	tta	ggg	ggg	caa	gag	tta	ttg	tat	ttt	1788
Leu	Thr	Gln	Tyr	Leu	Tyr	Gly	Leu	Gly	Gly	Gln	Glu	Leu	Leu	Tyr	Phe	
	560					565					570					
aaa	ata	tcg	caa	ctc	atc	aat	ctt	gac	gat	aaa	gtt	tcg	ccc	ttt	aga	1836
Lys	Ile	Ser	Gln	Leu	Ile	Asn	Leu	Asp	Asp	Lys	Val	Ser	Pro	Phe	Arg	
575					580					585					590	
atg	cca	cta	gag	agc	aag	atc	ggg	ttt	tcg	ccc	tta	acg	gga	ttg	aac	1884
Met	Pro	Leu	Glu	Ser	Lys	Ile	Gly	Phe	Ser	Pro	Leu	Thr	Gly	Leu	Asn	
				595					600					605		
atc	ttt	ggg	aat	gtc	ttt	tat	tcg	ttt	tat	caa	aac	cgc	tta	gaa	gaa	1932
Ile	Phe	Gly	Asn	Val	Phe	Tyr	Ser	Phe	Tyr	Gln	Asn	Arg	Leu	Glu	Glu	
			610					615					620			
atc	tct	gtg	aac	gcc	aat	tac	caa	cgc	aag	ttt	tta	agc	ttt	aac	ctc	1980
Ile	Ser	Val	Asn	Ala	Asn	Tyr	Gln	Arg	Lys	Phe	Leu	Ser	Phe	Asn	Leu	
		625					630					635				
tct	tat	ttt	tta	aaa	aac	aat	ttt	agc	agt	ggg	att	aat	agc	att	gta	2028
Ser	Tyr	Phe	Leu	Lys	Asn	Asn	Phe	Ser	Ser	Gly	Ile	Asn	Ser	Ile	Val	
	640					645					650					

gaa aat ctg cgg att att taaaggcggg ttttagcaac gactttggct
 Glu Asn Leu Arg Ile Ile
 655 660

2076

atttttccat gagcgcggat g

2097

<210> 38
 <211> 660
 <212> PRT
 <213> Helicobacter pylori

<400> 38
 Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
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 Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
 20 25 30
 Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
 35 40 45
 Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
 50 55 60
 Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
 65 70 75 80
 Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
 85 90 95
 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
 100 105 110
 Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
 115 120 125
 Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
 130 135 140
 Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
 145 150 155 160
 Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr
 165 170 175
 Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr
 180 185 190
 Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser
 195 200 205
 Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys
 210 215 220
 Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly
 225 230 235 240
 Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg
 245 250 255
 Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys
 260 265 270
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser
 275 280 285
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile
 290 295 300
 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr
 305 310 315 320
 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met
 325 330 335
 Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu
 340 345 350
 Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr
 355 360 365

Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu
 370 375 380
 Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr
 385 390 395 400
 Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro
 405 410 415
 Val Gly Leu Gln Phe Ser Leu Phe Lys Tyr Leu Ser Leu Gly Leu
 420 425 430
 Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn
 435 440 445
 Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe
 450 455 460
 Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu
 465 470 475 480
 Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile
 485 490 495
 Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala
 500 505 510
 Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp
 515 520 525
 Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser
 530 535 540
 Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr
 545 550 555 560
 Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile
 565 570 575
 Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro
 580 585 590
 Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe
 595 600 605
 Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser
 610 615 620
 Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr
 625 630 635 640
 Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn
 645 650 655
 Leu Arg Ile Ile
 660

<210> 39
 <211> 961
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (168)...(764)

<400> 39
 atgccgatta aatgcatgct gattaaatga atgaaaagag tccaaaccac cgcctttaac 60
 gcaccacgct tgaaattaaa actaaatttt agtgtattct tagcaaattt tagataagat 120
 caagcgtgat tttttctaaa ttttaggcac ttaaggaatc agtggttt atg aca agc 176
 Met Thr Ser
 1

gct ctg tta ggc tta caa att gtt tta gcg gta ttg att gtg gtg gtg 224
 Ala Leu Leu Gly Leu Gln Ile Val Leu Ala Val Leu Ile Val Val Val
 5 10 15

gtt ttg ttg caa aaa agt tct agc atc ggc tta ggg gct tat agc ggg	272
Val Leu Leu Gln Lys Ser Ser Ser Ile Gly Leu Gly Ala Tyr Ser Gly	
20 25 30 35	
agt aat gag tct tta ttt ggc gct aaa ggg cct gca agc ttt atg gcg	320
Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Ser Phe Met Ala	
40 45 50	
aaa tta acc atg ttt tta ggg ctg tta ttt gtc atc aac acc atc gct	368
Lys Leu Thr Met Phe Leu Gly Leu Leu Phe Val Ile Asn Thr Ile Ala	
55 60 65	
ttg ggc tat ttt tac aac aaa gaa tac ggc aag agc gtt tta gat gag	416
Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Val Leu Asp Glu	
70 75 80	
act aaa acc aac aaa gaa ctt tcg ccc cta gtc cct gcc acc ggc acg	464
Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala Thr Gly Thr	
85 90 95	
ctt aac cct gca ctt aat ccc aca tta aac cca acg ctc aac cct tta	512
Leu Asn Pro Ala Leu Asn Pro Thr Leu Asn Pro Thr Leu Asn Pro Leu	
100 105 110 115	
gag caa gcc cca act aat cct tta atg cca caa caa acg cct aac gaa	560
Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Gln Gln Thr Pro Asn Glu	
120 125 130	
ctc cct aaa gag cca gcc aaa acg cct tct gtt gaa agc ccc aaa cag	608
Leu Pro Lys Glu Pro Ala Lys Thr Pro Ser Val Glu Ser Pro Lys Gln	
135 140 145	
aat gaa aag aat gaa aag aat gac gcc aaa gag aat ggt ata aag ggt	656
Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly Ile Lys Gly	
150 155 160	
gtt gaa aaa acc aaa gag aac gcc aaa acg ccc cca acc acc cac caa	704
Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr Thr His Gln	
165 170 175	
aag cct aaa acg cat gca acg caa acc aac gcc cat acc aac caa aaa	752
Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr Asn Gln Lys	
180 185 190 195	
aag gat gaa aaa taatgttaca ggccatttat aacgaaacca aagatctgat	804
Lys Asp Glu Lys	
gcaaaaaagc attcaagctt taaacagggga tttttccact ctaaggagcg cgaaagtttc	864
agtcaatatt ttagatcaca tcaaagtggga ttattacggc acgcccacgg cattaaatca	924
agtcggatcc gtgatgagct tggatgcgac caccctt	961

<210> 40
 <211> 199
 <212> PRT
 <213> Helicobacter pylori

<400> 40

Met	Thr	Ser	Ala	Leu	Leu	Gly	Leu	Gln	Ile	Val	Leu	Ala	Val	Leu	Ile
1				5				10						15	
Val	Val	Val	Val	Leu	Leu	Gln	Lys	Ser	Ser	Ser	Ile	Gly	Leu	Gly	Ala
			20				25						30		
Tyr	Ser	Gly	Ser	Asn	Glu	Ser	Leu	Phe	Gly	Ala	Lys	Gly	Pro	Ala	Ser
		35				40						45			
Phe	Met	Ala	Lys	Leu	Thr	Met	Phe	Leu	Gly	Leu	Leu	Phe	Val	Ile	Asn
	50					55					60				
Thr	Ile	Ala	Leu	Gly	Tyr	Phe	Tyr	Asn	Lys	Glu	Tyr	Gly	Lys	Ser	Val
65					70					75					80
Leu	Asp	Glu	Thr	Lys	Thr	Asn	Lys	Glu	Leu	Ser	Pro	Leu	Val	Pro	Ala
				85				90						95	
Thr	Gly	Thr	Leu	Asn	Pro	Ala	Leu	Asn	Pro	Thr	Leu	Asn	Pro	Thr	Leu
			100					105					110		
Asn	Pro	Leu	Glu	Gln	Ala	Pro	Thr	Asn	Pro	Leu	Met	Pro	Gln	Gln	Thr
		115					120					125			
Pro	Asn	Glu	Leu	Pro	Lys	Glu	Pro	Ala	Lys	Thr	Pro	Ser	Val	Glu	Ser
		130				135					140				
Pro	Lys	Gln	Asn	Glu	Lys	Asn	Glu	Lys	Asn	Asp	Ala	Lys	Glu	Asn	Gly
145					150					155					160
Ile	Lys	Gly	Val	Glu	Lys	Thr	Lys	Glu	Asn	Ala	Lys	Thr	Pro	Pro	Thr
				165				170						175	
Thr	His	Gln	Lys	Pro	Lys	Thr	His	Ala	Thr	Gln	Thr	Asn	Ala	His	Thr
			180					185					190		
Asn	Gln	Lys	Lys	Asp	Glu	Lys									
			195												

<210> 41
 <211> 1058
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (325)... (879)

<400> 41
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 caacccttta gagcaagccc caactaatcc tttaatgccca caacaaacgc ctaacgaact 120
 ccctaaagag ccagccaaaa cgccttctgt tgaaagcccc aaacagaatg aaaagaatga 180
 aaagaatgac gccaaagaga atggtataaa ggggtgtgaa aaaaccaaag agaacgccaa 240
 aacgccccca accaccacc aaaagcctaa aacgcacgca acgcaaacca acgcccatac 300
 caaccaaaaa aaggatgaaa aata atg tta cag gcc att tat aac gaa acc 351
 Met Leu Gln Ala Ile Tyr Asn Glu Thr
 1 5
 aaa gat ctg atg caa aaa agc att caa gct tta aac agg gat ttt tcc 399
 Lys Asp Leu Met Gln Lys Ser Ile Gln Ala Leu Asn Arg Asp Phe Ser
 10 15 20 25
 act cta agg agc gcg aaa gtt tca gtc aat att tta gat cac atc aaa 447
 Thr Leu Arg Ser Ala Lys Val Ser Val Asn Ile Leu Asp His Ile Lys
 30 35 40
 gtg gat tat tac ggc acg ccc acg gca tta aat caa gtc gga tcc gtg 495
 Val Asp Tyr Tyr Gly Thr Pro Thr Ala Leu Asn Gln Val Gly Ser Val
 45 50 55

atg agc ttg gat gcg acc acc ctt caa atc agc cca tgg gaa aaa aac	543
Met Ser Leu Asp Ala Thr Thr Leu Gln Ile Ser Pro Trp Glu Lys Asn	
60 65 70	
ctg ctc aaa gaa att gaa aga tcc att caa gaa gcc aat att ggt gtc	591
Leu Leu Lys Glu Ile Glu Arg Ser Ile Gln Glu Ala Asn Ile Gly Val	
75 80 85	
aat cct aat aac gac ggc gaa acg atc aag ctt ttt ttc ccg ccc atg	639
Asn Pro Asn Asn Asp Gly Glu Thr Ile Lys Leu Phe Phe Pro Pro Met	
90 95 100 105	
aca agt gag caa aga aaa ctc atc gca aaa gac gcc aaa gcg atg ggt	687
Thr Ser Glu Gln Arg Lys Leu Ile Ala Lys Asp Ala Lys Ala Met Gly	
110 115 120	
gaa aag gct aaa gtg gct gtg agg aat atc cgc caa gat gct aac aac	735
Glu Lys Ala Lys Val Ala Val Arg Asn Ile Arg Gln Asp Ala Asn Asn	
125 130 135	
cag gtg aaa aaa tta gaa aaa gac aaa gaa atc agc gaa gat gaa agc	783
Gln Val Lys Lys Leu Glu Lys Asp Lys Glu Ile Ser Glu Asp Glu Ser	
140 145 150	
aaa aaa gcc caa gag cag atc caa aaa atc acc gat gaa gcc att aaa	831
Lys Lys Ala Gln Glu Gln Ile Gln Lys Ile Thr Asp Glu Ala Ile Lys	
155 160 165	
aaa att gat gaa agc gtg aaa aac aaa gaa gac gcg atc tta aag gtc	879
Lys Ile Asp Glu Ser Val Lys Asn Lys Glu Asp Ala Ile Leu Lys Val	
170 175 180 185	
taaaccatgg atattaaggc atgttatcaa aacgctaaag cggtattaga ggggcatttc	939
ttgctcagca gtgggtttca ttccaattat tatttgcaat ccgctaaagt tttagaagat	999
cccaaactag ccgaacaatt agcgctagaa ttagccaaac aaatccaaga agctcattt	1058

<210> 42
 <211> 185
 <212> PRT
 <213> Helicobacter pylori

<400> 42

Met Leu Gln Ala Ile Tyr Asn Glu Thr Lys Asp Leu Met Gln Lys Ser	
1 5 10 15	
Ile Gln Ala Leu Asn Arg Asp Phe Ser Thr Leu Arg Ser Ala Lys Val	
20 25 30	
Ser Val Asn Ile Leu Asp His Ile Lys Val Asp Tyr Tyr Gly Thr Pro	
35 40 45	
Thr Ala Leu Asn Gln Val Gly Ser Val Met Ser Leu Asp Ala Thr Thr	
50 55 60	
Leu Gln Ile Ser Pro Trp Glu Lys Asn Leu Leu Lys Glu Ile Glu Arg	
65 70 75 80	
Ser Ile Gln Glu Ala Asn Ile Gly Val Asn Pro Asn Asn Asp Gly Glu	
85 90 95	
Thr Ile Lys Leu Phe Phe Pro Pro Met Thr Ser Glu Gln Arg Lys Leu	
100 105 110	
Ile Ala Lys Asp Ala Lys Ala Met Gly Glu Lys Ala Lys Val Ala Val	
115 120 125	
Arg Asn Ile Arg Gln Asp Ala Asn Asn Gln Val Lys Lys Leu Glu Lys	

130 135 140
 Asp Lys Glu Ile Ser Glu Asp Glu Ser Lys Lys Ala Gln Glu Gln Ile
 145 150 155 160
 Gln Lys Ile Thr Asp Glu Ala Ile Lys Lys Ile Asp Glu Ser Val Lys
 165 170 175
 Asn Lys Glu Asp Ala Ile Leu Lys Val
 180 185

<210> 43
 <211> 1669
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (163)...(1389)

<400> 43
 gagtggatga aaaagacact ttcaattttg caaaaattgg ctatgaacag ggcaagggcg 60
 aagaattaaa agaagtagaa gaaaagcatg cgtttaagaa aatccctttt gtcaaagatt 120
 tgcacaaaat cgccccact atcttaaaaa agaggctata aa atg gct caa aat 174
 Met Ala Gln Asn
 1

ttc acg aaa ctc aac ccc cag ttt gaa aac atc att ttt gaa cat gac 222
 Phe Thr Lys Leu Asn Pro Gln Phe Glu Asn Ile Ile Phe Glu His Asp
 5 10 15 20

gac aac caa atg att tta aac ttt ggc ccc caa cac ccc agt agt cat 270
 Asp Asn Gln Met Ile Leu Asn Phe Gly Pro Gln His Pro Ser Ser His
 25 30 35

ggg caa ttg cgc ttg att ttg gaa tta gag ggc gaa aaa atc att aag 318
 Gly Gln Leu Arg Leu Ile Leu Glu Leu Glu Gly Glu Lys Ile Ile Lys
 40 45 50

gct acc cct gaa att ggc tac ttg cat aga ggc tgt gaa aag tta ggc 366
 Ala Thr Pro Glu Ile Gly Tyr Leu His Arg Gly Cys Glu Lys Leu Gly
 55 60 65

gaa aac atg acc tat aac gaa tac atg ccc act act gat aga ttg gat 414
 Glu Asn Met Thr Tyr Asn Glu Tyr Met Pro Thr Thr Asp Arg Leu Asp
 70 75 80

tac act tct tct acc agc aat aat tac gct tac gct tat gcg gta gag 462
 Tyr Thr Ser Ser Thr Ser Asn Asn Tyr Ala Tyr Ala Tyr Ala Val Glu
 85 90 95 100

acc tta ctc aat tta gaa atc cca cgc cga gcg cag gtg atc cgc acg 510
 Thr Leu Leu Asn Leu Glu Ile Pro Arg Arg Ala Gln Val Ile Arg Thr
 105 110 115

att tta cta gag ctt aac cgc atg atc tca cac atc ttt ttt atc agc 558
 Ile Leu Leu Glu Leu Asn Arg Met Ile Ser His Ile Phe Phe Ile Ser
 120 125 130

gtg cat gct tta gat gtg ggg gcg atg agc gtg ttt ttg tat gcg ttt 606
 Val His Ala Leu Asp Val Gly Ala Met Ser Val Phe Leu Tyr Ala Phe

135					140					145							
aaa	acg	agg	gaa	tac	ggc	ttg	gat	ttg	atg	gag	gat	tat	tgc	ggg	gct	654	
Lys	Thr	Arg	Glu	Tyr	Gly	Leu	Asp	Leu	Met	Glu	Asp	Tyr	Cys	Gly	Ala		
150					155					160							
agg	ctc	acg	cat	aac	gct	ata	agg	att	ggg	ggc	gtg	cct	tta	gat	tta	702	
Arg	Leu	Thr	His	Asn	Ala	Ile	Arg	Ile	Gly	Gly	Val	Pro	Leu	Asp	Leu		
165					170					175					180		
ccc	cct	aat	tgg	tta	gaa	ggc	tta	aaa	aag	ttt	tta	ggc	gaa	atg	agg	750	
Pro	Pro	Asn	Trp	Leu	Glu	Gly	Leu	Lys	Lys	Phe	Leu	Gly	Glu	Met	Arg		
185					190					195							
gaa	tgc	aaa	aaa	ctc	att	caa	ggc	tta	ttg	gat	aag	aat	cgc	att	tgg	798	
Glu	Cys	Lys	Lys	Leu	Ile	Gln	Gly	Leu	Leu	Asp	Lys	Asn	Arg	Ile	Trp		
200					205					210							
cgg	atg	cgc	ttg	gaa	aat	gtg	ggc	gtt	gta	acg	caa	aaa	atg	gcg	caa	846	
Arg	Met	Arg	Leu	Glu	Asn	Val	Gly	Val	Val	Thr	Gln	Lys	Met	Ala	Gln		
215					220					225							
agc	tgg	ggc	atg	agc	ggt	atc	atg	tta	aga	ggg	act	ggg	atc	gct	tat	894	
Ser	Trp	Gly	Met	Ser	Gly	Ile	Met	Leu	Arg	Gly	Thr	Gly	Ile	Ala	Tyr		
230					235					240							
gac	atc	aga	aaa	gaa	gag	cct	tat	gag	ctt	tat	aaa	gag	ctt	gat	ttt	942	
Asp	Ile	Arg	Lys	Glu	Glu	Pro	Tyr	Glu	Leu	Tyr	Lys	Glu	Leu	Asp	Phe		
245					250					255					260		
gat	gtg	ccg	gtg	ggc	aat	tat	ggc	gat	agt	tat	gat	agg	tat	tgt	ttg	990	
Asp	Val	Pro	Val	Gly	Asn	Tyr	Gly	Asp	Ser	Tyr	Asp	Arg	Tyr	Cys	Leu		
265					270					275							
tat	atg	tta	gaa	att	gat	gaa	agc	gtt	cgc	atc	att	gaa	cag	ctc	att	1038	
Tyr	Met	Leu	Glu	Ile	Asp	Glu	Ser	Val	Arg	Ile	Ile	Glu	Gln	Leu	Ile		
280					285					290							
cct	atg	tat	gct	aaa	acc	gat	acg	cct	atc	atg	gct	caa	aac	ccg	cat	1086	
Pro	Met	Tyr	Ala	Lys	Thr	Asp	Thr	Pro	Ile	Met	Ala	Gln	Asn	Pro	His		
295					300					305							
tat	att	tcc	gcc	cct	aaa	gaa	gat	ata	atg	acg	caa	aac	tac	gcc	ttg	1134	
Tyr	Ile	Ser	Ala	Pro	Lys	Glu	Asp	Ile	Met	Thr	Gln	Asn	Tyr	Ala	Leu		
310					315					320							
atg	cag	cat	ttt	gtt	tta	gtg	gct	cag	ggc	atg	cgt	ccg	ccc	gtt	ggg	1182	
Met	Gln	His	Phe	Val	Leu	Val	Ala	Gln	Gly	Met	Arg	Pro	Pro	Val	Gly		
325					330					335					340		
gaa	gtg	tat	gcc	ccc	aca	gaa	agc	cct	aaa	ggg	gaa	tta	ggg	ttt	ttt	1230	
Glu	Val	Tyr	Ala	Pro	Thr	Glu	Ser	Pro	Lys	Gly	Glu	Leu	Gly	Phe	Phe		
345					350					355							
atc	cat	tca	gag	ggc	gag	cct	tac	cct	cac	agg	cta	aaa	atc	aga	gcc	1278	
Ile	His	Ser	Glu	Gly	Glu	Pro	Tyr	Pro	His	Arg	Leu	Lys	Ile	Arg	Ala		
360					365					370							
cct	agc	ttt	tat	cac	att	ggg	gct	ttg	agc	gac	att	tta	gtg	ggg	caa	1326	

Pro Ser Phe Tyr His Ile Gly Ala Leu Ser Asp Ile Leu Val Gly Gln
 375 380 385

tat tta gcg gat gca gta acc gtg att ggc tca acc aat gcg gtg ttt 1374
 Tyr Leu Ala Asp Ala Val Thr Val Ile Gly Ser Thr Asn Ala Val Phe
 390 395 400

ggc gag gtg gat aga tgaaacgctt tgatttacgc cccttaaaag cgggtatttt 1429
 Gly Glu Val Asp Arg
 405

tgaacgctta gaagaattga ttgaaaaaga aatgcaacct aatgaagtcg ctattttcat 1489
 gtttgaagtg ggggattttt ctaatatccc taagagcgct gaatttatcc aatctaaagg 1549
 gcatgagctc ctcaattctt tgcgtttcaa tcaagcggat tggacgattg tcgtgagaaa 1609
 aaagcgttga ttttgagcgg ctttaacccc ttaaattctc ccttagtcgc aagctcttct 1669

<210> 44
 <211> 409
 <212> PRT
 <213> Helicobacter pylori

<400> 44
 Met Ala Gln Asn Phe Thr Lys Leu Asn Pro Gln Phe Glu Asn Ile Ile
 1 5 10 15
 Phe Glu His Asp Asp Asn Gln Met Ile Leu Asn Phe Gly Pro Gln His
 20 25 30
 Pro Ser Ser His Gly Gln Leu Arg Leu Ile Leu Glu Leu Glu Gly Glu
 35 40 45
 Lys Ile Ile Lys Ala Thr Pro Glu Ile Gly Tyr Leu His Arg Gly Cys
 50 55 60
 Glu Lys Leu Gly Glu Asn Met Thr Tyr Asn Glu Tyr Met Pro Thr Thr
 65 70 75 80
 Asp Arg Leu Asp Tyr Thr Ser Ser Thr Ser Asn Asn Tyr Ala Tyr Ala
 85 90 95
 Tyr Ala Val Glu Thr Leu Leu Asn Leu Glu Ile Pro Arg Arg Ala Gln
 100 105 110
 Val Ile Arg Thr Ile Leu Leu Glu Leu Asn Arg Met Ile Ser His Ile
 115 120 125
 Phe Phe Ile Ser Val His Ala Leu Asp Val Gly Ala Met Ser Val Phe
 130 135 140
 Leu Tyr Ala Phe Lys Thr Arg Glu Tyr Gly Leu Asp Leu Met Glu Asp
 145 150 155 160
 Tyr Cys Gly Ala Arg Leu Thr His Asn Ala Ile Arg Ile Gly Gly Val
 165 170 175
 Pro Leu Asp Leu Pro Pro Asn Trp Leu Glu Gly Leu Lys Lys Phe Leu
 180 185 190
 Gly Glu Met Arg Glu Cys Lys Lys Leu Ile Gln Gly Leu Leu Asp Lys
 195 200 205
 Asn Arg Ile Trp Arg Met Arg Leu Glu Asn Val Gly Val Val Thr Gln
 210 215 220
 Lys Met Ala Gln Ser Trp Gly Met Ser Gly Ile Met Leu Arg Gly Thr
 225 230 235 240
 Gly Ile Ala Tyr Asp Ile Arg Lys Glu Glu Pro Tyr Glu Leu Tyr Lys
 245 250 255
 Glu Leu Asp Phe Asp Val Pro Val Gly Asn Tyr Gly Asp Ser Tyr Asp
 260 265 270
 Arg Tyr Cys Leu Tyr Met Leu Glu Ile Asp Glu Ser Val Arg Ile Ile
 275 280 285

Glu Gln Leu Ile Pro Met Tyr Ala Lys Thr Asp Thr Pro Ile Met Ala
 290 295 300
 Gln Asn Pro His Tyr Ile Ser Ala Pro Lys Glu Asp Ile Met Thr Gln
 305 310 315 320
 Asn Tyr Ala Leu Met Gln His Phe Val Leu Val Ala Gln Gly Met Arg
 325 330 335
 Pro Pro Val Gly Glu Val Tyr Ala Pro Thr Glu Ser Pro Lys Gly Glu
 340 345 350
 Leu Gly Phe Phe Ile His Ser Glu Gly Glu Pro Tyr Pro His Arg Leu
 355 360 365
 Lys Ile Arg Ala Pro Ser Phe Tyr His Ile Gly Ala Leu Ser Asp Ile
 370 375 380
 Leu Val Gly Gln Tyr Leu Ala Asp Ala Val Thr Val Ile Gly Ser Thr
 385 390 395 400
 Asn Ala Val Phe Gly Glu Val Asp Arg
 405

<210> 45
 <211> 869
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (358)...(732)

<400> 45
 taacttggtg ttaactaccg ccagactcct tttgagtttg gcaaacgcgc caatgagttc 60
 tttaggcatt ttttcagtgc cgatcttaaa gttttcaaga ctgcgttgcg tttgagcccc 120
 ccaatatttg ctatcattta ctttgatttc gcccatcggt tcatgttcaa ttctaaattg 180
 catgctaata ctttgaaatt tgattttaaa accttaaaaa aatagcataa actcttatac 240
 cttctactta aaaaccctaa ttttttaaac accattttcca caatttttac acaaaagagg 300
 gttattatcc gttcgcaaca agaattttct tgttatctta atgtaaaggt caaaacg atg 360
 Met
 1

aaa aag tta gcc gct tta ttt tta gta agc gtg ttg ggg gtt atg ggt 408
 Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly
 5 10 15

tta aac gca tgg gag caa acc cta aaa gct aat gac ttg gaa gtg aaa 456
 Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys
 20 25 30

atc aaa tcc gtg ggt aac ccc att aaa ggc gat aac act ttc att ctc 504
 Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu
 35 40 45

agc ccc act tta aaa ggt aag gct tta gaa aaa gct atc gtt agg gtg 552
 Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val
 50 55 60 65

cag ttt atg atg cct gaa atg ccc ggc atg cca gcg atg aaa gaa atg 600
 Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met
 70 75 80

gcg caa gtg agt gaa aaa aac ggc ctt tat gaa gct aaa acc aat ctt 648
 Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu

85 90 95
tct atg aac ggg aca tgg cag gtt agg gtg gat att aaa tct aaa gag 696
Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu
100 105 110

ggt cag gtt tat cgc gct aaa aca agc ctg gat tta taagagcatg 742
Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
115 120 125

ctatcttttta taagcgcgtt tgataaaaagg ggcgttttcaa tacgcctttt aacagccttg 802
ttactgcttt ttagtttggg tttggctaaa gatttagaga tccaatcttt tgtggctaaa 862
taccttt 869

<210> 46
<211> 125
<212> PRT
<213> Helicobacter pylori

<400> 46
Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
1 5 10 15
Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
20 25 30
Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
35 40 45
Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
50 55 60
Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
65 70 75 80
Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
85 90 95
Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
100 105 110
Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
115 120 125

<210> 47
<211> 1217
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (73)...(1152)

<400> 47
tccatgcgtt ttgatgcatg tttaaaaaat ctttgggtat tttagcatgc caatgggttaa 60
aaaaaggtgg tt atg aat ggt ttt tgc gct aga cta cga gcc ata act cat 111
Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr His
1 5 10

aat gaa aga tta aaa atg aaa ata gcg gta tta ctc agt ggg ggg gtg 159
Asn Glu Arg Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val
15 20 25

gat agc tct tat agc gct tat agc tta aaa gag caa ggg cat gaa tta 207
Asp Ser Ser Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu

30	35	40	45	
gtg ggg att tat tta aaa ctc cat gcg agt gaa aaa aag cat gat tta	255			
Val Gly Ile Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu				
50 55 60				
tac atc aaa aac gct caa aaa gca tgc gag ttt tta ggc att cct tta	303			
Tyr Ile Lys Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro Leu				
65 70 75				
gag gtg ttg gat ttt caa aag gat ttt aaa agc gcg gtt tat gat gaa	351			
Glu Val Leu Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp Glu				
80 85 90				
ttt atc aac gcc tat gaa gaa ggg caa acc cca aac cct tgt gcg ttg	399			
Phe Ile Asn Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala Leu				
95 100 105				
tgc aac cct tta atg aag ttt ggg cta gct ttg gat cac gct tta aaa	447			
Cys Asn Pro Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu Lys				
110 115 120 125				
tta ggg tgt gaa aag atc gct acc ggg cat tat gcg aga gtc aaa gaa	495			
Leu Gly Cys Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys Glu				
130 135 140				
att gac aaa ata agt tat att caa gag gct ttg gat aaa act aaa gat	543			
Ile Asp Lys Ile Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys Asp				
145 150 155				
cag agc tat ttt tta tac gct tta gag cat gaa gtg atc gct aaa ttg	591			
Gln Ser Tyr Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys Leu				
160 165 170				
gtg ttc cct tta ggg gat ttg cta aaa aag gat att aag cct tta gcc	639			
Val Phe Pro Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu Ala				
175 180 185				
ttg aat gcg atg cct ttt tta ggc act tta gag act tat aag gaa tct	687			
Leu Asn Ala Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu Ser				
190 195 200 205				
caa gaa atc tgc ttt gtg gaa aaa agc tac att gac act tta aaa aag	735			
Gln Glu Ile Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys Lys				
210 215 220				
cat gtt gaa gtg gaa aaa gag ggc gtg gtg aaa aac cta caa ggc gaa	783			
His Val Glu Val Glu Lys Glu Gly Val Val Lys Asn Leu Gln Gly Glu				
225 230 235				
gtc att ggc acg cat aaa ggc tat atg caa tac acg att ggc aaa cgc	831			
Val Ile Gly Thr His Lys Gly Tyr Met Gln Tyr Thr Ile Gly Lys Arg				
240 245 250				
aaa ggc ttt agt att aaa ggc gcg tta gag ccg cat ttt gtg gtg ggg	879			
Lys Gly Phe Ser Ile Lys Gly Ala Leu Glu Pro His Phe Val Val Gly				
255 260 265				
att gac gct aaa aag aac gag cta gtc gtg ggc aaa aaa gaa gat ctc	927			

Ile Asp Ala Lys Lys Asn Glu Leu Val Val Gly Lys Lys Glu Asp Leu
 270 275 280 285
 gcc acg cat tcg ctt aag gct aaa aac aaa tct tta atg aaa gat ttt 975
 Ala Thr His Ser Leu Lys Ala Lys Asn Lys Ser Leu Met Lys Asp Phe
 290 295 300
 aaa gat ggc gaa tat ttt atc aag gct cgt tac agg agc gtg cct gct 1023
 Lys Asp Gly Glu Tyr Phe Ile Lys Ala Arg Tyr Arg Ser Val Pro Ala
 305 310 315
 aaa gcg cat gtg agt ttg aaa gat gag gtg att gaa gtg ggg ttt aaa 1071
 Lys Ala His Val Ser Leu Lys Asp Glu Val Ile Glu Val Gly Phe Lys
 320 325 330
 gag cct ttt tat ggc gtg gct aaa ggg caa gct ttg gtc gtt tat aaa 1119
 Glu Pro Phe Tyr Gly Val Ala Lys Gly Gln Ala Leu Val Val Tyr Lys
 335 340 345
 gat gac atc ttg ctt ggt ggg ggc gtg att gtt taaaaactaa agaactaaga 1172
 Asp Asp Ile Leu Leu Gly Gly Gly Val Ile Val
 350 355 360
 gatacgctt ttggcagtct cttaatgttt tattgaatag gcgtt 1217
 <210> 48
 <211> 360
 <212> PRT
 <213> Helicobacter pylori
 <400> 48
 Met Asn Gly Phe Cys Ala Arg Leu Arg Ala Ile Thr His Asn Glu Arg
 1 5 10 15
 Leu Lys Met Lys Ile Ala Val Leu Leu Ser Gly Gly Val Asp Ser Ser
 20 25 30
 Tyr Ser Ala Tyr Ser Leu Lys Glu Gln Gly His Glu Leu Val Gly Ile
 35 40 45
 Tyr Leu Lys Leu His Ala Ser Glu Lys Lys His Asp Leu Tyr Ile Lys
 50 55 60
 Asn Ala Gln Lys Ala Cys Glu Phe Leu Gly Ile Pro Leu Glu Val Leu
 65 70 75 80
 Asp Phe Gln Lys Asp Phe Lys Ser Ala Val Tyr Asp Glu Phe Ile Asn
 85 90 95
 Ala Tyr Glu Glu Gly Gln Thr Pro Asn Pro Cys Ala Leu Cys Asn Pro
 100 105 110
 Leu Met Lys Phe Gly Leu Ala Leu Asp His Ala Leu Lys Leu Gly Cys
 115 120 125
 Glu Lys Ile Ala Thr Gly His Tyr Ala Arg Val Lys Glu Ile Asp Lys
 130 135 140
 Ile Ser Tyr Ile Gln Glu Ala Leu Asp Lys Thr Lys Asp Gln Ser Tyr
 145 150 155 160
 Phe Leu Tyr Ala Leu Glu His Glu Val Ile Ala Lys Leu Val Phe Pro
 165 170 175
 Leu Gly Asp Leu Leu Lys Lys Asp Ile Lys Pro Leu Ala Leu Asn Ala
 180 185 190
 Met Pro Phe Leu Gly Thr Leu Glu Thr Tyr Lys Glu Ser Gln Glu Ile
 195 200 205
 Cys Phe Val Glu Lys Ser Tyr Ile Asp Thr Leu Lys Lys His Val Glu
 210 215 220

Val	Glu	Lys	Glu	Gly	Val	Val	Lys	Asn	Leu	Gln	Gly	Glu	Val	Ile	Gly
225					230					235					240
Thr	His	Lys	Gly	Tyr	Met	Gln	Tyr	Thr	Ile	Gly	Lys	Arg	Lys	Gly	Phe
			245						250						255
Ser	Ile	Lys	Gly	Ala	Leu	Glu	Pro	His	Phe	Val	Val	Gly	Ile	Asp	Ala
			260					265					270		
Lys	Lys	Asn	Glu	Leu	Val	Val	Gly	Lys	Lys	Glu	Asp	Leu	Ala	Thr	His
		275					280					285			
Ser	Leu	Lys	Ala	Lys	Asn	Lys	Ser	Leu	Met	Lys	Asp	Phe	Lys	Asp	Gly
	290					295					300				
Glu	Tyr	Phe	Ile	Lys	Ala	Arg	Tyr	Arg	Ser	Val	Pro	Ala	Lys	Ala	His
305					310					315					320
Val	Ser	Leu	Lys	Asp	Glu	Val	Ile	Glu	Val	Gly	Phe	Lys	Glu	Pro	Phe
			325					330						335	
Tyr	Gly	Val	Ala	Lys	Gly	Gln	Ala	Leu	Val	Val	Tyr	Lys	Asp	Asp	Ile
		340						345					350		
Leu	Leu	Gly	Gly	Gly	Val	Ile	Val								
		355					360								

<210> 49
 <211> 975
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (191)...(793)

<400> 49
 acattacaca tatctgtcgc taaaacgcgc cgtttcacta aaccactga ttgtaaaaat 60
 ttgtctattc gcatgcgttt atttaccct attctttaag tttttatcca taacttataa 120
 gggttttagt ttttagcatgt tagcattcag ccaccactct ttttaaggaa tttgtttgaa 180
 gtttcaaatt atg agt ttg tta gcc act ctt tta tta gcc tct tgc ttg 229
 Met Ser Leu Leu Ala Thr Leu Leu Leu Ala Ser Cys Leu
 1 5 10

ccc ccc aaa ggc cat cat tct ggt ttg gtg aat ctt tat atc gct cat 277
 Pro Pro Lys Gly His His Ser Gly Leu Val Asn Leu Tyr Ile Ala His
 15 20 25

caa ggc caa agc gtg cgc act tat tgg cgc aaa gtg gat aga gga gtt 325
 Gln Gly Gln Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg Gly Val
 30 35 40 45

atc gct aaa cac aat gaa gcg ctt aaa aaa gat cct aaa gca aag ctc 373
 Ile Ala Lys His Asn Glu Ala Leu Lys Lys Asp Pro Lys Ala Lys Leu
 50 55 60

aaa gac ccc agg ggg cct tta ttc atg cta ggg agt gag cgc ttc atg 421
 Lys Asp Pro Arg Gly Pro Leu Phe Met Leu Gly Ser Glu Arg Phe Met
 65 70 75

ctt tta tgg aaa aac cgc tac gct tta gcc aag ccc caa tcg ttc agg 469
 Leu Leu Trp Lys Asn Arg Tyr Ala Leu Ala Lys Pro Gln Ser Phe Arg
 80 85 90

cta gag cct ggt ttt tat tac ttg gat tct ttt agc gtg gaa act caa 517
 Leu Glu Pro Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu Thr Gln

95	100	105	
aaa ggc gtc ttg cag agc gct cct ggc tat tca tat act aaa aat ggc			565
Lys Gly Val Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly			
110	115	120	125
tat gat ttc aaa aac aac cgc ccc ttt ttc ctg gcc ttt gaa gtc aaa			613
Tyr Asp Phe Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys			
	130	135	140
cct gat ggc aaa acc att ctt cct agc gtg gaa tta agc ctg att aaa			661
Pro Asp Gly Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys			
	145	150	155
acc cct aga ggc ttt tta ggg gtg ttc ttg ttt gat aat aat gaa aag			709
Thr Pro Arg Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys			
	160	165	170
ggg act aac gcc aag tgg att gag ggg agt ttg aat tta aag ctt aaa			757
Gly Thr Asn Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys			
	175	180	185
aac gct tcc ttt aaa gat gcg tgg ggg ttg gaa caa taaagcatga			803
Asn Ala Ser Phe Lys Asp Ala Trp Gly Leu Glu Gln			
190	195	200	
agtgatcgct tgcttttcgt aagctcttta tgattagatt gtaaaaaaat gccttgagta			863
tttttttagat tttattaccc ctattcaatt ggaacaaagc cattaatatt ttaaaaaactt			923
ttaaaaacga taaacataat ccgcgctcca agtaacatag ctttcaaaaa tg			975

<210> 50
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 50
Met Ser Leu Leu Ala Thr Leu Leu Leu Ala Ser Cys Leu Pro Pro Lys
1 5 10 15
Gly His His Ser Gly Leu Val Asn Leu Tyr Ile Ala His Gln Gly Gln
20 25 30
Ser Val Arg Thr Tyr Trp Arg Lys Val Asp Arg Gly Val Ile Ala Lys
35 40 45
His Asn Glu Ala Leu Lys Lys Asp Pro Lys Ala Lys Leu Lys Asp Pro
50 55 60
Arg Gly Pro Leu Phe Met Leu Gly Ser Glu Arg Phe Met Leu Leu Trp
65 70 75 80
Lys Asn Arg Tyr Ala Leu Ala Lys Pro Gln Ser Phe Arg Leu Glu Pro
85 90 95
Gly Phe Tyr Tyr Leu Asp Ser Phe Ser Val Glu Thr Gln Lys Gly Val
100 105 110
Leu Gln Ser Ala Pro Gly Tyr Ser Tyr Thr Lys Asn Gly Tyr Asp Phe
115 120 125
Lys Asn Asn Arg Pro Phe Phe Leu Ala Phe Glu Val Lys Pro Asp Gly
130 135 140
Lys Thr Ile Leu Pro Ser Val Glu Leu Ser Leu Ile Lys Thr Pro Arg
145 150 155 160
Gly Phe Leu Gly Val Phe Leu Phe Asp Asn Asn Glu Lys Gly Thr Asn
165 170 175
Ala Lys Trp Ile Glu Gly Ser Leu Asn Leu Lys Leu Lys Asn Ala Ser

180 185 190
Phe Lys Asp Ala Trp Gly Leu Glu Gln
195 200

<210> 51
<211> 1116
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (90)...(1076)

<400> 51
tataaatata tcgttttcatt agcgaattta atggcggttaa gcgatcatat tgatttattt 60
tatgaatttg tttattaagg gaaaaaatc atg tca aat agc atg ttg gat aaa 113
Met Ser Asn Ser Met Leu Asp Lys
1 5
aat aaa gcg att ctt aca ggg ggt ggg gct tta tta tta ggg cta atc 161
Asn Lys Ala Ile Leu Thr Gly Gly Gly Ala Leu Leu Leu Gly Leu Ile
10 15 20
gtg ctt ttt tat tta gct tat cgc cct aag gct gaa gtg ttg caa ggg 209
Val Leu Phe Tyr Leu Ala Tyr Arg Pro Lys Ala Glu Val Leu Gln Gly
25 30 35 40
ttt ttg gaa gcc aga gaa tac agc gtg agc tcc aaa gtc cct ggc cgc 257
Phe Leu Glu Ala Arg Glu Tyr Ser Val Ser Ser Lys Val Pro Gly Arg
45 50 55
att gaa aag gtg ttt gtt aaa aaa ggc gat cac att aaa aag ggc gat 305
Ile Glu Lys Val Phe Val Lys Lys Gly Asp His Ile Lys Lys Gly Asp
60 65 70
ttg gtt ttt agc att tct agc cct gaa tta gaa gcc aaa ctc gct caa 353
Leu Val Phe Ser Ile Ser Ser Pro Glu Leu Glu Ala Lys Leu Ala Gln
75 80 85
gct gaa gcc ggg cat aaa gcc gct aaa gcg ctt agc gat gaa gtc aaa 401
Ala Glu Ala Gly His Lys Ala Ala Lys Ala Leu Ser Asp Glu Val Lys
90 95 100
aga ggc tca aga gac gaa acg att aat tct gcg aga gac gtt tgg caa 449
Arg Gly Ser Arg Asp Glu Thr Ile Asn Ser Ala Arg Asp Val Trp Gln
105 110 115 120
gca gcc aaa tcc caa gcc act tta gcc aaa gag act tat aag cgc gtt 497
Ala Ala Lys Ser Gln Ala Thr Leu Ala Lys Glu Thr Tyr Lys Arg Val
125 130 135
caa gat ttg tat gat aat ggc gtg gcg agc ttg caa aag cgc gat gaa 545
Gln Asp Leu Tyr Asp Asn Gly Val Ala Ser Leu Gln Lys Arg Asp Glu
140 145 150
gcc tat gcg gct tat gaa agc act aaa tac aac gag agc gcg gct tac 593
Ala Tyr Ala Ala Tyr Glu Ser Thr Lys Tyr Asn Glu Ser Ala Ala Tyr
155 160 165

caa aag tat aaa atg gct tta ggg ggg gcg agc tct gaa agt aag att	641
Gln Lys Tyr Lys Met Ala Leu Gly Gly Ala Ser Ser Glu Ser Lys Ile	
170 175 180	
gcc gct aag gct aaa gag agc gcg gct tta ggg caa gtg aat gaa gtg	689
Ala Ala Lys Ala Lys Glu Ser Ala Ala Leu Gly Gln Val Asn Glu Val	
185 190 195 200	
gag tct tat tta aaa gac gtc aaa gcg aca gcc cca att gat ggg gaa	737
Glu Ser Tyr Leu Lys Asp Val Lys Ala Thr Ala Pro Ile Asp Gly Glu	
205 210 215	
gtg agt aac gtg ctt tta agc ggt ggc gag ctt agc cct aag ggt ttt	785
Val Ser Asn Val Leu Leu Ser Gly Gly Glu Leu Ser Pro Lys Gly Phe	
220 225 230	
cct gtg gtt tta atg ata gat tta aag gat agt tgg tta aaa atc agc	833
Pro Val Val Leu Met Ile Asp Leu Lys Asp Ser Trp Leu Lys Ile Ser	
235 240 245	
gtg cct gaa aag tat ttg aac gag ttt aaa gtg ggt aag gaa ttt gaa	881
Val Pro Glu Lys Tyr Leu Asn Glu Phe Lys Val Gly Lys Glu Phe Glu	
250 255 260	
ggc tat atc ccg gcg ttg aaa aaa agc acg aaa ttc agg gtc aaa tat	929
Gly Tyr Ile Pro Ala Leu Lys Lys Ser Thr Lys Phe Arg Val Lys Tyr	
265 270 275 280	
ttg agc gtg atg ggg gat ttt gcg act tgg aaa gcg acg aat aat tcc	977
Leu Ser Val Met Gly Asp Phe Ala Thr Trp Lys Ala Thr Asn Asn Ser	
285 290 295	
aac act tac gac atg aaa agc tat gaa gtg gaa gcc ata ccc tta gaa	1025
Asn Thr Tyr Asp Met Lys Ser Tyr Glu Val Glu Ala Ile Pro Leu Glu	
300 305 310	
gag ttg gaa aat ttt agg gta ggg atg agc gtg tta gtt acc att aaa	1073
Glu Leu Glu Asn Phe Arg Val Gly Met Ser Val Leu Val Thr Ile Lys	
315 320 325	
cct taaaaaggat tgttttgttc agattgataa gcgcattgggt	1116
Pro	

<210> 52
 <211> 329
 <212> PRT
 <213> Helicobacter pylori

<400> 52
 Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly
 1 5 10 15
 Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg
 20 25 30
 Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser
 35 40 45
 Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys

50		55		60
Gly Asp His Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro				
65		70		75
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala				
	85		90	
Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile				
	100		105	
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu				
	115		120	
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val				
	130		135	
Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Tyr Glu Ser Thr				
	145		150	
Lys Tyr Asn Glu Ser Ala Ala Tyr Gln Lys Tyr Lys Met Ala Leu Gly				
	165		170	
Gly Ala Ser Ser Glu Ser Lys Ile Ala Ala Lys Ala Lys Glu Ser Ala				
	180		185	
Ala Leu Gly Gln Val Asn Glu Val Glu Ser Tyr Leu Lys Asp Val Lys				
	195		200	
Ala Thr Ala Pro Ile Asp Gly Glu Val Ser Asn Val Leu Leu Ser Gly				
	210		215	
Gly Glu Leu Ser Pro Lys Gly Phe Pro Val Val Leu Met Ile Asp Leu				
	225		230	
Lys Asp Ser Trp Leu Lys Ile Ser Val Pro Glu Lys Tyr Leu Asn Glu				
	245		250	
Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Lys				
	260		265	
Ser Thr Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala				
	275		280	
Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr				
	290		295	
Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly				
	305		310	
Met Ser Val Leu Val Thr Ile Lys Pro			315	
				320
				325

<210> 53
 <211> 1514
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (94)...(1467)

<400> 53
 aaataaaata ggcatacatta taacatgttg ctttttaagt gaaagcggtta agttgttagg 60
 gtatagtggc ttaaaaattt taggatattg aga atg ctt gaa act tct agc cat 114
 Met Leu Glu Thr Ser Ser His
 1 5

ttt tta aaa tcg ttt cgc ttg aag cgt tat ata ggg ttt tta ttg att 162
 Phe Leu Lys Ser Phe Arg Leu Lys Arg Tyr Ile Gly Phe Leu Leu Ile
 10 15 20

tct tta gcg tta tta atc acg ccc ttt gtt cgc att gat ggg gcg cat 210
 Ser Leu Ala Leu Leu Ile Thr Pro Phe Val Arg Ile Asp Gly Ala His
 25 30 35

ttg ttt ttg atc tct ttt gag cat aag caa ctg cat ttt tta ggc aag	258
Leu Phe Leu Ile Ser Phe Glu His Lys Gln Leu His Phe Leu Gly Lys	
40 45 50 55	
atc ttt agc gct gaa gaa ttg caa gtc atg cct ttt atg gtt att ttg	306
Ile Phe Ser Ala Glu Glu Leu Gln Val Met Pro Phe Met Val Ile Leu	
60 65 70	
ctt ttt ata ggg att ttt ttc atc acc act agc ctt ggg cgt gtg tgg	354
Leu Phe Ile Gly Ile Phe Phe Ile Thr Thr Ser Leu Gly Arg Val Trp	
75 80 85	
tgc ggt tgg gct tgc ccg caa acc ttt tta agg gtg ctt tat aga gat	402
Cys Gly Trp Ala Cys Pro Gln Thr Phe Leu Arg Val Leu Tyr Arg Asp	
90 95 100	
gtg att gaa acc aag att ttc aaa ctc cat aaa aag atc agc aac aag	450
Val Ile Glu Thr Lys Ile Phe Lys Leu His Lys Lys Ile Ser Asn Lys	
105 110 115	
caa gaa agc cct aaa aac acc cca agc tac aag atc cgt aaa gta ttg	498
Gln Glu Ser Pro Lys Asn Thr Pro Ser Tyr Lys Ile Arg Lys Val Leu	
120 125 130 135	
agc gtt tta ttg ttc gct cct gtt gtg gcg ggg cta atg atg ttg ttt	546
Ser Val Leu Leu Phe Ala Pro Val Val Ala Gly Leu Met Met Leu Phe	
140 145 150	
ttc ttt tat ttc atc gcc cca gaa gat ttt ttt atg tat ctt aaa aac	594
Phe Phe Tyr Phe Ile Ala Pro Glu Asp Phe Phe Met Tyr Leu Lys Asn	
155 160 165	
cct agc gat cac cct att gct atg ggt ttt tgg ctt ttt agc acg gct	642
Pro Ser Asp His Pro Ile Ala Met Gly Phe Trp Leu Phe Ser Thr Ala	
170 175 180	
gtg gtg cta ttt gat ata gtg gtg gtt gcg gag cgt ttt tgc att tat	690
Val Val Leu Phe Asp Ile Val Val Val Ala Glu Arg Phe Cys Ile Tyr	
185 190 195	
tta tgc cct tac gct agg gtg caa tcg gtg ttg tat gac aat gac acc	738
Leu Cys Pro Tyr Ala Arg Val Gln Ser Val Leu Tyr Asp Asn Asp Thr	
200 205 210 215	
tta aac cct att tat gat gaa aag cgc ggc gga gcg ctt tat aat aat	786
Leu Asn Pro Ile Tyr Asp Glu Lys Arg Gly Gly Ala Leu Tyr Asn Asn	
220 225 230	
cag ggc cat ctc ttc ccc tta cct ccc aaa aaa cgc agc cca gaa aac	834
Gln Gly His Leu Phe Pro Leu Pro Pro Lys Lys Arg Ser Pro Glu Asn	
235 240 245	
gaa tgc gtg aat tgt ttg cat tgc gtg cag gtt tgc ccc acg cat att	882
Glu Cys Val Asn Cys Leu His Cys Val Gln Val Cys Pro Thr His Ile	
250 255 260	
gac atc agg aag ggc ttg caa tta gaa tgc atc aat tgt tta gaa tgc	930
Asp Ile Arg Lys Gly Leu Gln Leu Glu Cys Ile Asn Cys Leu Glu Cys	

265	270	275	
gtg gat gca tgc acg att acc atg gct aaa ttt aac cgc cct tca ctc			978
Val Asp Ala Cys Thr Ile Thr Met Ala Lys Phe Asn Arg Pro Ser Leu			
280	285	290	295
atc caa tgg tct tca act aac gct att aat acg cgc caa aaa gtg cac			1026
Ile Gln Trp Ser Ser Thr Asn Ala Ile Asn Thr Arg Gln Lys Val His			
	300	305	310
ctg gtg cgt tta aaa acg atc gct tac atg ggg gtt atc gct att gtg			1074
Leu Val Arg Leu Lys Thr Ile Ala Tyr Met Gly Val Ile Ala Ile Val			
	315	320	325
atc gct ctt tta gcc atc act tcg ttt aaa aaa gaa cgc atg ctc tta			1122
Ile Ala Leu Leu Ala Ile Thr Ser Phe Lys Lys Glu Arg Met Leu Leu			
	330	335	340
gac att aac cgc aac agc gat ctg tat gaa ttg cgc tct agc ggg tat			1170
Asp Ile Asn Arg Asn Ser Asp Leu Tyr Glu Leu Arg Ser Ser Gly Tyr			
	345	350	355
gtg gat aac gat tac gtg ttt tta ttc cac aac acg gac aat aaa gac			1218
Val Asp Asn Asp Tyr Val Phe Leu Phe His Asn Thr Asp Asn Lys Asp			
	360	365	370
cat gag ttt tat ttc aaa gtt tta ggg caa aaa gac att cag atc aaa			1266
His Glu Phe Tyr Phe Lys Val Leu Gly Gln Lys Asp Ile Gln Ile Lys			
	380	385	390
aag cct tta aat cct atc gcc att aaa gcc ggg caa aag att aaa gcg			1314
Lys Pro Leu Asn Pro Ile Ala Ile Lys Ala Gly Gln Lys Ile Lys Ala			
	395	400	405
gta gtg att tta aga aaa ccc cta aag agt aac gcc aca gaa tac aag			1362
Val Val Ile Leu Arg Lys Pro Leu Lys Ser Asn Ala Thr Glu Tyr Lys			
	410	415	420
aac gct aaa gac gct cta atc ccc att acc ata caa gct tat agc gcg			1410
Asn Ala Lys Asp Ala Leu Ile Pro Ile Thr Ile Gln Ala Tyr Ser Ala			
	425	430	435
gac gat aag aat att acg ata gaa agg gaa tcg gtg ttt att gca cca			1458
Asp Asp Lys Asn Ile Thr Ile Glu Arg Glu Ser Val Phe Ile Ala Pro			
	440	445	450
agt gag gat tgaagcctaa aactagcggtt caatcacttc ataaggcaag			1507
Ser Glu Asp			
ccttggtt			1514
<210> 54			
<211> 458			
<212> PRT			
<213> Helicobacter pylori			
<400> 54			
Met Leu Glu Thr Ser Ser His Phe Leu Lys Ser Phe Arg Leu Lys Arg			

1	5	10	15
Tyr Ile Gly Phe Leu Leu Ile Ser Leu Ala Leu Leu Ile Thr Pro Phe			
20	25	30	
Val Arg Ile Asp Gly Ala His Leu Phe Leu Ile Ser Phe Glu His Lys			
35	40	45	
Gln Leu His Phe Leu Gly Lys Ile Phe Ser Ala Glu Glu Leu Gln Val			
50	55	60	
Met Pro Phe Met Val Ile Leu Leu Phe Ile Gly Ile Phe Phe Ile Thr			
65	70	75	80
Thr Ser Leu Gly Arg Val Trp Cys Gly Trp Ala Cys Pro Gln Thr Phe			
85	90	95	
Leu Arg Val Leu Tyr Arg Asp Val Ile Glu Thr Lys Ile Phe Lys Leu			
100	105	110	
His Lys Lys Ile Ser Asn Lys Gln Glu Ser Pro Lys Asn Thr Pro Ser			
115	120	125	
Tyr Lys Ile Arg Lys Val Leu Ser Val Leu Leu Phe Ala Pro Val Val			
130	135	140	
Ala Gly Leu Met Met Leu Phe Phe Phe Tyr Phe Ile Ala Pro Glu Asp			
145	150	155	160
Phe Phe Met Tyr Leu Lys Asn Pro Ser Asp His Pro Ile Ala Met Gly			
165	170	175	
Phe Trp Leu Phe Ser Thr Ala Val Val Leu Phe Asp Ile Val Val Val			
180	185	190	
Ala Glu Arg Phe Cys Ile Tyr Leu Cys Pro Tyr Ala Arg Val Gln Ser			
195	200	205	
Val Leu Tyr Asp Asn Asp Thr Leu Asn Pro Ile Tyr Asp Glu Lys Arg			
210	215	220	
Gly Gly Ala Leu Tyr Asn Asn Gln Gly His Leu Phe Pro Leu Pro Pro			
225	230	235	240
Lys Lys Arg Ser Pro Glu Asn Glu Cys Val Asn Cys Leu His Cys Val			
245	250	255	
Gln Val Cys Pro Thr His Ile Asp Ile Arg Lys Gly Leu Gln Leu Glu			
260	265	270	
Cys Ile Asn Cys Leu Glu Cys Val Asp Ala Cys Thr Ile Thr Met Ala			
275	280	285	
Lys Phe Asn Arg Pro Ser Leu Ile Gln Trp Ser Ser Thr Asn Ala Ile			
290	295	300	
Asn Thr Arg Gln Lys Val His Leu Val Arg Leu Lys Thr Ile Ala Tyr			
305	310	315	320
Met Gly Val Ile Ala Ile Val Ile Ala Leu Leu Ala Ile Thr Ser Phe			
325	330	335	
Lys Lys Glu Arg Met Leu Leu Asp Ile Asn Arg Asn Ser Asp Leu Tyr			
340	345	350	
Glu Leu Arg Ser Ser Gly Tyr Val Asp Asn Asp Tyr Val Phe Leu Phe			
355	360	365	
His Asn Thr Asp Asn Lys Asp His Glu Phe Tyr Phe Lys Val Leu Gly			
370	375	380	
Gln Lys Asp Ile Gln Ile Lys Lys Pro Leu Asn Pro Ile Ala Ile Lys			
385	390	395	400
Ala Gly Gln Lys Ile Lys Ala Val Val Ile Leu Arg Lys Pro Leu Lys			
405	410	415	
Ser Asn Ala Thr Glu Tyr Lys Asn Ala Lys Asp Ala Leu Ile Pro Ile			
420	425	430	
Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg			
435	440	445	
Glu Ser Val Phe Ile Ala Pro Ser Glu Asp			
450	455		

<210> 55
 <211> 990
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (228)...(782)

<400> 55
 acgatttgat caataacgaa aataaaattg atgaaatcaa taatgaagaa aacgctgac 60
 cttcgcaaaa aagaacgaac aacgttttgc aacgagccac taaccaccaa gacaatctca 120
 attccccact caacaggaag tattaagtg tgaaactttt ttcaaaggat ttatttataaa 180
 aagtaacccc tttattttta agcgtttatt ttttaaacc caccatt atg caa gcc 236
 Met Gln Ala
 1

aaa agc cgt ttt tat gtg gct tct caa tac cag gtg ggg aaa atg atc 284
 Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly Lys Met Ile
 5 10 15

atg aaa aaa tac aac gat ctc aaa cgc acg att gaa ggg gcg agc ttt 332
 Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly Ala Ser Phe
 20 25 30 35

tct tta ggc tgg gag att aac ccc act aac tac tgg ttt tat tgc cgc 380
 Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe Tyr Ser Arg
 40 45 50

tat tac ttt ttt atg gat tac ggg aat gtc att ctc aat aaa aga acg 428
 Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn Lys Arg Thr
 55 60 65

ggc gct caa gcg aac atg ttc act tat ggc ttt ggg ggg gat ttg att 476
 Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly Asp Leu Ile
 70 75 80

gtg gaa tac aat aaa aac ccc ttg tat gta ttt tct ctt ttt tat ggc 524
 Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu Phe Tyr Gly
 85 90 95

atg caa gtt gct gaa aac aca tgg acg att tcc aaa cac agc gcg aat 572
 Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His Ser Ala Asn
 100 105 110 115

ttc atc att gac gat tgg cgc agc att caa ggg ttt tgc ctc aaa act 620
 Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser Leu Lys Thr
 120 125 130

tcc aat ttt agg atg ttg ggt tta gtg ggg ttt aaa ttc caa acc gtg 668
 Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe Gln Thr Val
 135 140 145

cta ttc cac cat gac gca agt att gaa gtg ggg atc aaa tgg cct ttt 716
 Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys Trp Pro Phe
 150 155 160

gct ttt gaa tac gac tca gcc ttt gta agg ctt ttt tct gtc ttt att 764
 Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser Val Phe Ile

165

170

175

tcg cac act ttc tac ctt taaactaatt ccaaccctac cgggcaatga 812
 Ser His Thr Phe Tyr Leu
 180 185

tgcgtcccta aaatatcttt atagattaaa gcgtctttta agcgcgtttt taaagggtta 872
 gagcataaaa aataatcaat gcgccaacca atgtttttat cccttgcttg ttgcatgtaa 932
 ctccaccagg tgtaagcctt ttctttgtta gggtaaaaat aacggaaagt gtcaataa 990

<210> 56
 <211> 185
 <212> PRT
 <213> Helicobacter pylori

<400> 56
 Met Gln Ala Lys Ser Arg Phe Tyr Val Ala Ser Gln Tyr Gln Val Gly
 1 5 10 15
 Lys Met Ile Met Lys Lys Tyr Asn Asp Leu Lys Arg Thr Ile Glu Gly
 20 25 30
 Ala Ser Phe Ser Leu Gly Trp Glu Ile Asn Pro Thr Asn Tyr Trp Phe
 35 40 45
 Tyr Ser Arg Tyr Tyr Phe Phe Met Asp Tyr Gly Asn Val Ile Leu Asn
 50 55 60
 Lys Arg Thr Gly Ala Gln Ala Asn Met Phe Thr Tyr Gly Phe Gly Gly
 65 70 75 80
 Asp Leu Ile Val Glu Tyr Asn Lys Asn Pro Leu Tyr Val Phe Ser Leu
 85 90 95
 Phe Tyr Gly Met Gln Val Ala Glu Asn Thr Trp Thr Ile Ser Lys His
 100 105 110
 Ser Ala Asn Phe Ile Ile Asp Asp Trp Arg Ser Ile Gln Gly Phe Ser
 115 120 125
 Leu Lys Thr Ser Asn Phe Arg Met Leu Gly Leu Val Gly Phe Lys Phe
 130 135 140
 Gln Thr Val Leu Phe His His Asp Ala Ser Ile Glu Val Gly Ile Lys
 145 150 155 160
 Trp Pro Phe Ala Phe Glu Tyr Asp Ser Ala Phe Val Arg Leu Phe Ser
 165 170 175
 Val Phe Ile Ser His Thr Phe Tyr Leu
 180 185

<210> 57
 <211> 1161
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (109)...(1113)

<400> 57
 atcttacctt tatcttttaa gattttatga aaaatagttt catttttact attgttattt 60
 tcttagtaat gttataatcg ctttataaat catacaaaaa ggatcgct atg tta gtt 117
 Met Leu Val
 1

act cgc ttt aaa aaa gct ttc att tct tat tct tta ggc gtg ctt gtc 165
 Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly Val Leu Val

5	10	15	
gct tca tta tgg ttg aac gtg tgc aac gct tca gcg caa gaa gtc aaa	213		
Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln Glu Val Lys			
20 25 30 35			
gtc aag gat tat ttc ggg gag caa acc atc aag ctt cct gtt tct aaa	261		
Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro Val Ser Lys			
40 45 50			
ata gcc tat ata ggg agc tat gta gaa gtg cct gcc atg ctt aat gtt	309		
Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met Leu Asn Val			
55 60 65			
tgg aat agg gtt gta ggc gtt tgc gat tac gct ttt aaa gac gat att	357		
Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys Asp Asp Ile			
70 75 80			
gtc aaa gcc act ctc aaa ggc gaa gat ctt aaa cgc gtc aaa cac atg	405		
Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val Lys His Met			
85 90 95			
agc act gat cat aca gcc gcg cta aat gta gag ctt tta aaa aag ctt	453		
Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu Lys Lys Leu			
100 105 110 115			
agc cct gat ctt gtg gta acc ttt gtg ggc aac cct aaa gcg gta gag	501		
Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val Glu			
120 125 130			
cat gcg aaa aaa ttt ggt ata tca ttt ctt tct ttt caa gag aca acg	549		
His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln Glu Thr Thr			
135 140 145			
att gca gag gcc atg cag gcc atg caa gct caa gcc acg gtt tta gag	597		
Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr Val Leu Glu			
150 155 160			
att gac gct tcc aaa aaa ttc gcc aaa atg caa gaa act ttg gat ttt	645		
Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr Leu Asp Phe			
165 170 175			
att gct gag cgt ttg aaa aat gtc aaa aag aaa aag ggg gtg gag ctt	693		
Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly Val Glu Leu			
180 185 190 195			
ttc cat aaa gcc aat aaa atc agc ggc cat caa gcc att agc tca gac	741		
Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile Ser Ser Asp			
200 205 210			
att tta gaa aaa ggg ggc ata gac aat ttt ggc ttg aaa tat gtc aaa	789		
Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val Lys			
215 220 225			
ttt ggg cgt gct gac att agc gtg gaa aaa atc gtt aaa gaa aac cct	837		
Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn Pro			
230 235 240			
gag att atc ttt att tgg tgg ata agc cca ctc acg cct gaa gat gtg	885		

Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp Val
 245 250 255
 tta aac aac ccc aaa ttt gct acc atc aaa gcc att aaa aac aag cag 933
 Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys Gln
 260 265 270 275
 gtt tat aaa ctc ccc aca atg gat att ggc ggg cct aga gcc cca ctc 981
 Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro Leu
 280 285 290
 ata agt ctt ttt atc gct cta aaa gcc cac cct gaa gcc ttt aag ggc 1029
 Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys Gly
 295 300 305
 gtg gat att aat gcg atg gtt aaa gac tac tat aaa gtg gtt ttt gat 1077
 Val Asp Ile Asn Ala Met Val Lys Asp Tyr Tyr Lys Val Val Phe Asp
 310 315 320
 ttg aat gat gca gag gtt gag ccc ttt tta tgg cat taatttttaa 1123
 Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
 325 330 335
 aaaggggttg atgttttttag cctttcgtgt atcgcgct 1161

<210> 58
 <211> 335
 <212> PRT
 <213> Helicobacter pylori

<400> 58
 Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly
 1 5 10 15
 Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln
 20 25 30
 Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro
 35 40 45
 Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met
 50 55 60
 Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys
 65 70 75 80
 Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val
 85 90 95
 Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu
 100 105 110
 Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys
 115 120 125
 Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln
 130 135 140
 Glu Thr Thr Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr
 145 150 155 160
 Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr
 165 170 175
 Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly
 180 185 190
 Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile
 195 200 205
 Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys
 210 215 220

Tyr	Val	Lys	Phe	Gly	Arg	Ala	Asp	Ile	Ser	Val	Glu	Lys	Ile	Val	Lys
225					230					235					240
Glu	Asn	Pro	Glu	Ile	Ile	Phe	Ile	Trp	Trp	Ile	Ser	Pro	Leu	Thr	Pro
				245					250						255
Glu	Asp	Val	Leu	Asn	Asn	Pro	Lys	Phe	Ala	Thr	Ile	Lys	Ala	Ile	Lys
			260					265					270		
Asn	Lys	Gln	Val	Tyr	Lys	Leu	Pro	Thr	Met	Asp	Ile	Gly	Gly	Pro	Arg
		275					280					285			
Ala	Pro	Leu	Ile	Ser	Leu	Phe	Ile	Ala	Leu	Lys	Ala	His	Pro	Glu	Ala
	290					295					300				
Phe	Lys	Gly	Val	Asp	Ile	Asn	Ala	Met	Val	Lys	Asp	Tyr	Tyr	Lys	Val
305					310					315					320
Val	Phe	Asp	Leu	Asn	Asp	Ala	Glu	Val	Glu	Pro	Phe	Leu	Trp	His	
			325					330						335	

<210> 59
 <211> 800
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (121)...(669)

<400> 59
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 tgaaatcaaa caaagccaaa aagaaaagaa aaaattcccc actttcaaag gaggttttta 120
 atg cgt tgg tgg tgt ttt ttg gtg tgt tgt ttt ggt att tta agc gtg 168
 Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val
 1 5 10 15

atg gac gct aaa aaa tta gag aat aag aat ttg aaa aaa gaa aga gag 216
 Met Asp Ala Lys Lys Leu Glu Asn Lys Asn Leu Lys Lys Glu Arg Glu
 20 25 30

ctt tta gag att act ggc aac caa ttt gta gcg aac gac aaa acc aaa 264
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys
 35 40 45

acc gct gtt att caa ggc aat gtg cag atc aaa aag ggt aaa gac cgg 312
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg
 50 55 60

ttg ttt gcg gac aag gtg agc gtg ttt tta aac gat aaa cga aag cca 360
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro
 65 70 75 80

gag cgc tat gaa gcc aca ggg aac acg cat ttt aac atc ttt aca gag 408
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu
 85 90 95

gac aat cgt gaa atc agc ggg agt gct gac aag ctc att tat aac gcg 456
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala
 100 105 110

ctg aat ggg gaa tac aaa tta ttg caa aat gcg gtg gtt aga gaa gtg 504
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val
 115 120 125

ggg aaa tcc aat gtc atc acc ggc gat gaa atc att tta aac aaa act 552
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr
 130 135 140

aag ggt tat gct gat gtg ttg ggg agc gcg aaa cgg ccc gct aaa ttc 600
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe
 145 150 155 160

gtg ttt gat atg gaa gat att aat gaa gaa aat cgt aag gct aaa ttg 648
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu
 165 170 175

aag aag aaa ggc gaa aaa cca tgattgtcat taaagacgct cattttctca 699
 Lys Lys Lys Gly Glu Lys Pro
 180

cttcttcaag ccaacttttt caatgccctg cgagtttgac ttctgaaatg gtggttttag 759
 ggcgcagcaa tgtaggcaaa agctcgttta ttaatacctt g 800

<210> 60
 <211> 183
 <212> PRT
 <213> Helicobacter pylori

<400> 60
 Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val
 1 5 10 15
 Met Asp Ala Lys Lys Leu Glu Asn Lys Asn Leu Lys Lys Glu Arg Glu
 20 25 30
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys
 35 40 45
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg
 50 55 60
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro
 65 70 75 80
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu
 85 90 95
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala
 100 105 110
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val
 115 120 125
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr
 130 135 140
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe
 145 150 155 160
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu
 165 170 175
 Lys Lys Lys Gly Glu Lys Pro
 180

<210> 61
 <211> 724
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS

<222> (88)...(618)

<400> 61

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aaaaaaaggc taatactatc ataagga atg aag ttg ata aaa ttt gtg cgt aat 114
Met Lys Leu Ile Lys Phe Val Arg Asn
1 5

gtg gtt ttg ttc att tta acg gcg atc ttt tta gcg ttc atg ctt ttg 162
Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe Met Leu Leu
10 15 20 25

gtg agt tat tgc atg ccc cat tat agc gcg gct gtc att agc ggg gtg 210
Val Ser Tyr Cys Met Pro His Tyr Ser Ala Ala Val Ile Ser Gly Val
30 35 40

gaa gtc aaa aga atg aat gaa aat gaa aac acg ccc aat aat aag gaa 258
Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu
45 50 55

gta aaa acc ctt gct aga gat gtc tat ttt gtg caa act tac gac cct 306
Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro
60 65 70

aaa gat caa aaa agc gta acc gtt tat cgt aac gaa gac acg cgc ttt 354
Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe
75 80 85

agc ttc cct ttt tat ttt aag ttt aat tcg gct gat att tca gcc ctc 402
Ser Phe Pro Phe Tyr Phe Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu
90 95 100 105

gct caa agt tta atc aat cag caa gtg gaa gtg aaa tac tat ggt tgg 450
Ala Gln Ser Leu Ile Asn Gln Gln Val Glu Val Lys Tyr Tyr Gly Trp
110 115 120

cgg atc aat ttg ttt aac atg ttc cct aat gtg att ttt tta aag ccc 498
Arg Ile Asn Leu Phe Asn Met Phe Pro Asn Val Ile Phe Leu Lys Pro
125 130 135

tta aaa gag agc act gac att tca aag ccc att ttt agc tgg att tta 546
Leu Lys Glu Ser Thr Asp Ile Ser Lys Pro Ile Phe Ser Trp Ile Leu
140 145 150

tac gct ttg ctg tta atg ggc ttt ttt atc agc gcg cgt tct gtt tgc 594
Tyr Ala Leu Leu Leu Met Gly Phe Phe Ile Ser Ala Arg Ser Val Cys
155 160 165

act tta ttt aag agc aaa gct cat taaaactttt aggctttggtt ggaaaatcac 648
Thr Leu Phe Lys Ser Lys Ala His
170 175

aatgggggtta ttggagcgtg tattaaaaag ctcaatatag ggcaagctga tgctgtgaaa 708
agcgggtgttg tttcct 724

<210> 62

<211> 177

<212> PRT

<213> Helicobacter pylori

<400> 62
Met Lys Leu Ile Lys Phe Val Arg Asn Val Val Leu Phe Ile Leu Thr
1 5 10 15
Ala Ile Phe Leu Ala Phe Met Leu Leu Val Ser Tyr Cys Met Pro His
20 25 30
Tyr Ser Ala Val Ile Ser Gly Val Glu Val Lys Arg Met Asn Glu
35 40 45
Asn Glu Asn Thr Pro Asn Asn Lys Glu Val Lys Thr Leu Ala Arg Asp
50 55 60
Val Tyr Phe Val Gln Thr Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr
65 70 75 80
Val Tyr Arg Asn Glu Asp Thr Arg Phe Ser Phe Pro Phe Tyr Phe Lys
85 90 95
Phe Asn Ser Ala Asp Ile Ser Ala Leu Ala Gln Ser Leu Ile Asn Gln
100 105 110
Gln Val Glu Val Lys Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn Met
115 120 125
Phe Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Thr Asp Ile
130 135 140
Ser Lys Pro Ile Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Met Gly
145 150 155 160
Phe Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Ser Lys Ala
165 170 175
His

<210> 63
<211> 1041
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (162)...(896)

<400> 63
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tttttggttat tatgggactt gtgttttttg gttgcaccag taagggtgcat gagatgaaaa 120
aaagcccttg cacattgtta tgaaaacagg ttaaattctcg c atg aaa gaa aag cct 176
Met Lys Glu Lys Pro
1 5
ttc aat agc gag cag ttg atc tat tta gaa gag ctt tta aac cac caa 224
Phe Asn Ser Glu Gln Leu Ile Tyr Leu Glu Glu Leu Leu Asn His Gln
10 15 20
gaa aag cat tta gaa aac aag ctt tct ggt ttt tcg gtg aat gat ttg 272
Glu Lys His Leu Glu Asn Lys Leu Ser Gly Phe Ser Val Asn Asp Leu
25 30 35
gac atg caa agc gtg ttc aga ctg gag agg aac cgc ttg aaa atc gct 320
Asp Met Gln Ser Val Phe Arg Leu Glu Arg Asn Arg Leu Lys Ile Ala
40 45 50
tat aaa ctc tta ggc ttg atg agt ttt atc gct ctt gtt tta gcg atc 368
Tyr Lys Leu Leu Gly Leu Met Ser Phe Ile Ala Leu Val Leu Ala Ile
55 60 65

gtg tta atc agt gtt ctg ccc tta caa aaa acc gaa cac cat ttc gtg	416
Val Leu Ile Ser Val Leu Pro Leu Gln Lys Thr Glu His His Phe Val	
70 75 80 85	
gat ttt tta aat cag gac aag cat tac gcc att atc caa aga gcg gat	464
Asp Phe Leu Asn Gln Asp Lys His Tyr Ala Ile Ile Gln Arg Ala Asp	
90 95 100	
aaa agc att tcc agt aat gaa gcg ttg gct cgt tcg ctc att ggg gcg	512
Lys Ser Ile Ser Ser Asn Glu Ala Leu Ala Arg Ser Leu Ile Gly Ala	
105 110 115	
tat gtg tta aac cga gag agt att aac cgc att gac gat aaa tcg cgc	560
Tyr Val Leu Asn Arg Glu Ser Ile Asn Arg Ile Asp Asp Lys Ser Arg	
120 125 130	
tat gaa ttg gtg cgc ttg caa agc agt tct aaa gtg tgg caa cgc ttt	608
Tyr Glu Leu Val Arg Leu Gln Ser Ser Ser Lys Val Trp Gln Arg Phe	
135 140 145	
gaa gat ttg att aaa acc caa aac agc att tat gtg caa agc cat ttg	656
Glu Asp Leu Ile Lys Thr Gln Asn Ser Ile Tyr Val Gln Ser His Leu	
150 155 160 165	
gaa aga gaa gtc cat atc gtc aat att gcg atc tat cag caa gac aat	704
Glu Arg Glu Val His Ile Val Asn Ile Ala Ile Tyr Gln Gln Asp Asn	
170 175 180	
aac ccc att gcg agc gtc tcc att gcg gct aaa ctt ttg aac gaa aac	752
Asn Pro Ile Ala Ser Val Ser Ile Ala Ala Lys Leu Leu Asn Glu Asn	
185 190 195	
aag ttg gtg tat gaa aag cgt tat aaa atc gta ttg agt tat ttg ttt	800
Lys Leu Val Tyr Glu Lys Arg Tyr Lys Ile Val Leu Ser Tyr Leu Phe	
200 205 210	
gac acc ccg gat ttt gat tac gct tcc atg cct aaa aac cct acc gga	848
Asp Thr Pro Asp Phe Asp Tyr Ala Ser Met Pro Lys Asn Pro Thr Gly	
215 220 225	
ttt aaa atc acc cgt tac agc atc act gaa atc act aat agg ggt gat	896
Phe Lys Ile Thr Arg Tyr Ser Ile Thr Glu Ile Thr Asn Arg Gly Asp	
230 235 240 245	
tgatgcgtaa ggtttttatcac gctcttggtg gctttttggt ggctttttagc gcttttaaaag	956
ccgatgatttt tttagaagaa gcgaacgaaa cagccccggc gcattttaaac caccctatgc	1016
aggattttaaa cgccattcaa gggag	1041

<210> 64

<211> 245

<212> PRT

<213> Helicobacter pylori

<400> 64

Met Lys Glu Lys Pro Phe Asn Ser Glu Gln Leu Ile Tyr Leu Glu Glu	
1 5 10 15	
Leu Leu Asn His Gln Glu Lys His Leu Glu Asn Lys Leu Ser Gly Phe	
20 25 30	
Ser Val Asn Asp Leu Asp Met Gln Ser Val Phe Arg Leu Glu Arg Asn	

Asn	Gly	Asp	Ala	Lys	Lys	Phe	Ser	Thr	Leu	Val	Glu	Lys	Met	Arg	Phe	
65						70					75					
aac	tcc	ggt	ata	ttg	ggg	aat	tta	aga	gtg	cat	gca	cgt	ttg	agg	caa	467
Asn	Ser	Gly	Ile	Leu	Gly	Asn	Leu	Arg	Val	His	Ala	Arg	Leu	Arg	Gln	95
80					85					90						
gcc	cta	aaa	ttg	caa	aag	aat	ttg	aaa	tat	tgc	ctt	aaa	atc	atc	gct	515
Ala	Leu	Lys	Leu	Gln	Lys	Asn	Leu	Lys	Tyr	Cys	Leu	Lys	Ile	Ile	Ala	110
				100					105							
agg	gat	tct	ttt	tat	agc	tac	cgc	acc	ggt	att	tat	atc	ccc	tta	ggc	563
Arg	Asp	Ser	Phe	Tyr	Ser	Tyr	Arg	Thr	Gly	Ile	Tyr	Ile	Pro	Leu	Gly	125
			115					120								
att	tct	tta	aaa	gat	caa	aaa	acg	gct	caa	aaa	atg	ctc	gct	gat	ttg	611
Ile	Ser	Leu	Lys	Asp	Gln	Lys	Thr	Ala	Gln	Lys	Met	Leu	Ala	Asp	Leu	140
		130					135									
agc	gtg	gta	ggg	gcg	tat	ctt	aaa	aaa	caa	caa	gag	aat	gaa	aag	gct	659
Ser	Val	Val	Gly	Ala	Tyr	Leu	Lys	Lys	Gln	Gln	Glu	Asn	Glu	Lys	Ala	155
	145					150					155					
caa	agc	cct	tat	tac	aga	aac	aac	aac	tat	tac	aac	tct	tac	tat	agc	707
Gln	Ser	Pro	Tyr	Tyr	Arg	Asn	Asn	Asn	Tyr	Tyr	Asn	Ser	Tyr	Tyr	Ser	175
160					165					170						
cct	tat	tac	gga	atg	tat	ggt	atg	tat	ggc	atg	ggc	atg	tat	gga	atg	755
Pro	Tyr	Tyr	Gly	Met	Tyr	Gly	Met	Tyr	Gly	Met	Gly	Met	Tyr	Gly	Met	190
				180					185							
tat	ggc	atg	ggc	atg	tat	gat	ttt	tat	gac	ttt	tat	gat	ggc	atg	tat	803
Tyr	Gly	Met	Gly	Met	Tyr	Asp	Phe	Tyr	Asp	Phe	Tyr	Asp	Gly	Met	Tyr	205
			195					200								
gga	ttc	tac	cct	aac	atg	ttt	ttc	atg	atg	caa	gtt	caa	gat	tac	ttg	851
Gly	Phe	Tyr	Pro	Asn	Met	Phe	Phe	Met	Met	Gln	Val	Gln	Asp	Tyr	Leu	220
		210				215										
atg	tta	gaa	aat	tac	atg	tat	gcg	ctc	gat	caa	gaa	gag	att	tta	gat	899
Met	Leu	Glu	Asn	Tyr	Met	Tyr	Ala	Leu	Asp	Gln	Glu	Glu	Ile	Leu	Asp	235
	225					230					235					
cat	gac	gct	tct	act	gac	caa	ctt	gat	acg	cct	act	gat	gat	gac	aaa	947
His	Asp	Ala	Ser	Thr	Asp	Gln	Leu	Asp	Thr	Pro	Thr	Asp	Asp	Asp	Lys	255
240					245					250						
gac	gat	aaa	gac	gat	aaa	tcc	tta	cag	cag	gca	aat	ctt	atg	aac	ttt	995
Asp	Asp	Lys	Asp	Asp	Lys	Ser	Leu	Gln	Gln	Ala	Asn	Leu	Met	Asn	Phe	270
				260					265							
tat	cgt	gat	ccc	aaa	ttc	agc	aaa	ggc	att	caa	acc	aac	cgc	ttg	aat	1043
Tyr	Arg	Asp	Pro	Lys	Phe	Ser	Lys	Gly	Ile	Gln	Thr	Asn	Arg	Leu	Asn	285
			275					280								
agc	gct	tta	gtc	aat	tta	gac	aac	agt	cgc	atg	ctc	aaa	gac	aat	tcg	1091
Ser	Ala	Leu	Val	Asn	Leu	Asp	Asn	Ser	Arg	Met	Leu	Lys	Asp	Asn	Ser	300
		290					295					300				

ctt ttc cac act aaa gcc atg ccc act aaa agc gtg gat gcg ata act	1139
Leu Phe His Thr Lys Ala Met Pro Thr Lys Ser Val Asp Ala Ile Thr	
305 310 315	
tct caa gcc aaa gag ctt aac cat tta gtg ggg caa atc aaa gaa atg	1187
Ser Gln Ala Lys Glu Leu Asn His Leu Val Gly Gln Ile Lys Glu Met	
320 325 330 335	
aag caa gac ggg gcg agt cct agt aag att gat tca gtt gtc aat aaa	1235
Lys Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp Ser Val Val Asn Lys	
340 345 350	
gct atg gaa gtg agg gac aag cta gac aat aat ctc aac caa cta gac	1283
Ala Met Glu Val Arg Asp Lys Leu Asp Asn Asn Leu Asn Gln Leu Asp	
355 360 365	
aat gac tta aaa gat caa aaa ggg ctt tca agc gag caa caa gct caa	1331
Asn Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser Glu Gln Gln Ala Gln	
370 375 380	
gtg gat aaa gcc cta gac agc gtg caa caa tta agc cat agc agc gat	1379
Val Asp Lys Ala Leu Asp Ser Val Gln Gln Leu Ser His Ser Ser Asp	
385 390 395	
gtg gtg ggg aat tat tta gac ggg agt ttg aaa att gat ggc gat gat	1427
Val Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys Ile Asp Gly Asp Asp	
400 405 410 415	
aga gat gat ttg aat gat gcg atg aat aac cct atg caa caa ccc gtg	1475
Arg Asp Asp Leu Asn Asp Ala Met Asn Asn Pro Met Gln Gln Pro Val	
420 425 430	
caa caa acg cct act agc aac atg gcc gac acc cat gca aat gac agc	1523
Gln Gln Thr Pro Thr Ser Asn Met Ala Asp Thr His Ala Asn Asp Ser	
435 440 445	
aag gat caa ggg agt aac gcg ctc ata aac cct aac agc gcc act aac	1571
Lys Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro Asn Ser Ala Thr Asn	
450 455 460	
gcc gac gac act cac act gac gat act cac act gac act aac acc aca	1619
Ala Asp Asp Thr His Thr Asp Asp Thr His Thr Asp Thr Asn Thr Thr	
465 470 475	
aac gat gct agc acc act gac acc ccc act gac gat aaa gat gct agc	1667
Asn Asp Ala Ser Thr Thr Asp Thr Pro Thr Asp Asp Lys Asp Ala Ser	
480 485 490 495	
ggc ttg aac aat acc ggc gat atg aat aac acg gat acc ggc aac acg	1715
Gly Leu Asn Asn Thr Gly Asp Met Asn Asn Thr Asp Thr Gly Asn Thr	
500 505 510	
gac acc ggc aat acg gat acc ggt aac act gat gat atg agc aac atg	1763
Asp Thr Gly Asn Thr Asp Thr Gly Asn Thr Asp Asp Met Ser Asn Met	
515 520 525	
aac aac ggc aac gat gat acg ggt aac gct aat gac gac atg agc aac	1811
Asn Asn Gly Asn Asp Asp Thr Gly Asn Ala Asn Asp Asp Met Ser Asn	
530 535 540	

ggc aac gac atg ggc gat gat ttg aac aac gcg aac gat atg aac gac 1859
 Gly Asn Asp Met Gly Asp Asp Leu Asn Asn Ala Asn Asp Met Asn Asp
 545 550 555

gac atg ggt aat ggc aac gat gac atg ggc gat atg ggg gat atg aac 1907
 Asp Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn
 560 565 570 575

gac gat atg ggt ggc gat atg gga gac atg ggg gat atg ggc gat atg 1955
 Asp Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met
 580 585 590

ggg aat tgagattaac cccaatatca aagagtgata gccaaaactt taaggaatat 2011
 Gly Asn

ttttatagta aaaacgattc ttttaaggta atagggggga tattttgc 2059

<210> 66
 <211> 593
 <212> PRT
 <213> Helicobacter pylori

<400> 66
 Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn Ala
 1 5 10 15
 Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu Lys
 20 25 30
 Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser
 35 40 45
 Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn
 50 55 60
 Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn
 65 70 75 80
 Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala
 85 90 95
 Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg
 100 105 110
 Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly Ile
 115 120 125
 Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser
 130 135 140
 Val Val Gly Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala Gln
 145 150 155 160
 Ser Pro Tyr Tyr Arg Asn Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro
 165 170 175
 Tyr Tyr Gly Met Tyr Gly Met Tyr Gly Met Gly Met Tyr Gly Met Tyr
 180 185 190
 Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe Tyr Asp Gly Met Tyr Gly
 195 200 205
 Phe Tyr Pro Asn Met Phe Phe Met Met Gln Val Gln Asp Tyr Leu Met
 210 215 220
 Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln Glu Glu Ile Leu Asp His
 225 230 235 240
 Asp Ala Ser Thr Asp Gln Leu Asp Thr Pro Thr Asp Asp Asp Lys Asp
 245 250 255
 Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala Asn Leu Met Asn Phe Tyr
 260 265 270

atg gaa ttt gat gct gtt att att gga ggt ggg gtt tca ggg tgc gcg	165
Met Glu Phe Asp Ala Val Ile Ile Gly Gly Gly Val Ser Gly Cys Ala	
5 10 15	
acc ttt tat act ttg agc gaa tac agc tct tta aag cgc gtg gct atc	213
Thr Phe Tyr Thr Leu Ser Glu Tyr Ser Ser Leu Lys Arg Val Ala Ile	
20 25 30	
gtg gaa aaa tgc tct aaa ttg gct caa atc agc tcc agc gct aaa gct	261
Val Glu Lys Cys Ser Lys Leu Ala Gln Ile Ser Ser Ser Ala Lys Ala	
35 40 45 50	
aat tgc caa acc att cat gat ggc tct att gaa acg aat tac act ccc	309
Asn Ser Gln Thr Ile His Asp Gly Ser Ile Glu Thr Asn Tyr Thr Pro	
55 60 65	
gaa aaa gct aaa aaa gtg cgt ttg agc gct tat aag acc agg caa tac	357
Glu Lys Ala Lys Lys Val Arg Leu Ser Ala Tyr Lys Thr Arg Gln Tyr	
70 75 80	
gct ttg aat aaa ggc ttg caa aat gaa gtg att ttt gaa acc cag aaa	405
Ala Leu Asn Lys Gly Leu Gln Asn Glu Val Ile Phe Glu Thr Gln Lys	
85 90 95	
atg gct ata ggc gtg ggc gat gaa gaa tgc gag ttc atg aaa aaa cgc	453
Met Ala Ile Gly Val Gly Asp Glu Glu Cys Glu Phe Met Lys Lys Arg	
100 105 110	
tac gaa tct ttt aaa gaa atc ttt gtg ggg tta gaa gaa ttt gac aag	501
Tyr Glu Ser Phe Lys Glu Ile Phe Val Gly Leu Glu Glu Phe Asp Lys	
115 120 125 130	
caa aag att aaa gaa tta gag cct aat gtg att tta ggg gct aat ggc	549
Gln Lys Ile Lys Glu Leu Glu Pro Asn Val Ile Leu Gly Ala Asn Gly	
135 140 145	
ata gac agg cat gaa aac att atc ggg cat ggg tat aga aag gat tgg	597
Ile Asp Arg His Glu Asn Ile Ile Gly His Gly Tyr Arg Lys Asp Trp	
150 155 160	
agc acc atg aat ttt gcg aag ttg agt gaa aac ttc gtt gaa gaa gcc	645
Ser Thr Met Asn Phe Ala Lys Leu Ser Glu Asn Phe Val Glu Glu Ala	
165 170 175	
cta aaa tta aag cct aac aac cag gtg ttt ttg aat ttc aaa gtg aaa	693
Leu Lys Leu Lys Pro Asn Asn Gln Val Phe Leu Asn Phe Lys Val Lys	
180 185 190	
aag att gaa aaa cgc aac gac act tac gcc gta att tca gaa gac gct	741
Lys Ile Glu Lys Arg Asn Asp Thr Tyr Ala Val Ile Ser Glu Asp Ala	
195 200 205 210	
gaa gaa gtg tat gct aaa ttc gtg ctg gtc aat gcc ggc tct tac gct	789
Glu Glu Val Tyr Ala Lys Phe Val Leu Val Asn Ala Gly Ser Tyr Ala	
215 220 225	
ttg cct ttg gct cag agc atg ggc tat ggc cta gat tta ggg tgc ttg	837
Leu Pro Leu Ala Gln Ser Met Gly Tyr Gly Leu Asp Leu Gly Cys Leu	
230 235 240	

cct gtg gcg ggc agc ttt tat ttt gtg ccg gat tta tta agg ggt aag	885
Pro Val Ala Gly Ser Phe Tyr Phe Val Pro Asp Leu Leu Arg Gly Lys	
245 250 255	
gtt tat acc gtt caa aac ccc aaa ctc cct ttt gca gcc gtg cat ggc	933
Val Tyr Thr Val Gln Asn Pro Lys Leu Pro Phe Ala Ala Val His Gly	
260 265 270	
gac cct gat gcc gtc att aaa gga aaa aca cga atc ggg cct acc gct	981
Asp Pro Asp Ala Val Ile Lys Gly Lys Thr Arg Ile Gly Pro Thr Ala	
275 280 285 290	
tta acg atg cct aaa tta gaa cgc aac aaa tgt tgg ctt aag ggc att	1029
Leu Thr Met Pro Lys Leu Glu Arg Asn Lys Cys Trp Leu Lys Gly Ile	
295 300 305	
agc ttg gaa ttg ttg aaa atg gat ttg aat aaa gat gtg ttt aaa att	1077
Ser Leu Glu Leu Leu Lys Met Asp Leu Asn Lys Asp Val Phe Lys Ile	
310 315 320	
gcg ttt gat ttg atg agc gat aaa gaa atc cga aat tat gtg ttt aaa	1125
Ala Phe Asp Leu Met Ser Asp Lys Glu Ile Arg Asn Tyr Val Phe Lys	
325 330 335	
aac atg gtt ttt gaa ttg ccc att atc ggt aaa agg aaa ttt tta aaa	1173
Asn Met Val Phe Glu Leu Pro Ile Ile Gly Lys Arg Lys Phe Leu Lys	
340 345 350	
gac gct caa aaa atc atc ccc tct ctt agc cta gaa gat cta gaa tac	1221
Asp Ala Gln Lys Ile Ile Pro Ser Leu Ser Leu Glu Asp Leu Glu Tyr	
355 360 365 370	
gct cat ggt ttt ggt gaa gtg cgc ccg caa gtt tta gac aga acc aag	1269
Ala His Gly Phe Gly Glu Val Arg Pro Gln Val Leu Asp Arg Thr Lys	
375 380 385	
cga aaa ctg gaa tta ggc gaa aaa aag att tgc acc cat aaa ggc atc	1317
Arg Lys Leu Glu Leu Gly Glu Lys Lys Ile Cys Thr His Lys Gly Ile	
390 395 400	
act ttt aac atg acc cct tct cca ggc gcg acg agt tgt ttg caa aac	1365
Thr Phe Asn Met Thr Pro Ser Pro Gly Ala Thr Ser Cys Leu Gln Asn	
405 410 415	
gcc ctt gtg gat tcc caa gaa atc gct gcg tat ttg ggc gag agc ttt	1413
Ala Leu Val Asp Ser Gln Glu Ile Ala Ala Tyr Leu Gly Glu Ser Phe	
420 425 430	
gaa tta gaa cgc ttt tat aaa gat tta tcc cca gaa gaa ttg gaa aat	1461
Glu Leu Glu Arg Phe Tyr Lys Asp Leu Ser Pro Glu Glu Leu Glu Asn	
435 440 445 450	
taaaaacgca tgcaaaaaga acaagaagcc caagaatcg ctaaaaaagc cgttaaaatc	1521
gtgttt	1527

<210> 68
 <211> 450
 <212> PRT

<213> Helicobacter pylori

<400> 68

Met	Ser	Met	Glu	Phe	Asp	Ala	Val	Ile	Ile	Gly	Gly	Gly	Val	Ser	Gly	1	5	10	15
Cys	Ala	Thr	Phe	Tyr	Thr	Leu	Ser	Glu	Tyr	Ser	Ser	Leu	Lys	Arg	Val	20	25	30	
Ala	Ile	Val	Glu	Lys	Cys	Ser	Lys	Leu	Ala	Gln	Ile	Ser	Ser	Ser	Ala	35	40	45	
Lys	Ala	Asn	Ser	Gln	Thr	Ile	His	Asp	Gly	Ser	Ile	Glu	Thr	Asn	Tyr	50	55	60	
Thr	Pro	Glu	Lys	Ala	Lys	Lys	Val	Arg	Leu	Ser	Ala	Tyr	Lys	Thr	Arg	65	70	75	80
Gln	Tyr	Ala	Leu	Asn	Lys	Gly	Leu	Gln	Asn	Glu	Val	Ile	Phe	Glu	Thr	85	90	95	
Gln	Lys	Met	Ala	Ile	Gly	Val	Gly	Asp	Glu	Glu	Cys	Glu	Phe	Met	Lys	100	105	110	
Lys	Arg	Tyr	Glu	Ser	Phe	Lys	Glu	Ile	Phe	Val	Gly	Leu	Glu	Glu	Phe	115	120	125	
Asp	Lys	Gln	Lys	Ile	Lys	Glu	Leu	Glu	Pro	Asn	Val	Ile	Leu	Gly	Ala	130	135	140	
Asn	Gly	Ile	Asp	Arg	His	Glu	Asn	Ile	Ile	Gly	His	Gly	Tyr	Arg	Lys	145	150	155	160
Asp	Trp	Ser	Thr	Met	Asn	Phe	Ala	Lys	Leu	Ser	Glu	Asn	Phe	Val	Glu	165	170	175	
Glu	Ala	Leu	Lys	Leu	Lys	Pro	Asn	Asn	Gln	Val	Phe	Leu	Asn	Phe	Lys	180	185	190	
Val	Lys	Lys	Ile	Glu	Lys	Arg	Asn	Asp	Thr	Tyr	Ala	Val	Ile	Ser	Glu	195	200	205	
Asp	Ala	Glu	Glu	Val	Tyr	Ala	Lys	Phe	Val	Leu	Val	Asn	Ala	Gly	Ser	210	215	220	
Tyr	Ala	Leu	Pro	Leu	Ala	Gln	Ser	Met	Gly	Tyr	Gly	Leu	Asp	Leu	Gly	225	230	235	240
Cys	Leu	Pro	Val	Ala	Gly	Ser	Phe	Tyr	Phe	Val	Pro	Asp	Leu	Leu	Arg	245	250	255	
Gly	Lys	Val	Tyr	Thr	Val	Gln	Asn	Pro	Lys	Leu	Pro	Phe	Ala	Ala	Val	260	265	270	
His	Gly	Asp	Pro	Asp	Ala	Val	Ile	Lys	Gly	Lys	Thr	Arg	Ile	Gly	Pro	275	280	285	
Thr	Ala	Leu	Thr	Met	Pro	Lys	Leu	Glu	Arg	Asn	Lys	Cys	Trp	Leu	Lys	290	295	300	
Gly	Ile	Ser	Leu	Glu	Leu	Lys	Met	Asp	Leu	Asn	Lys	Asp	Val	Phe		305	310	315	320
Lys	Ile	Ala	Phe	Asp	Leu	Met	Ser	Asp	Lys	Glu	Ile	Arg	Asn	Tyr	Val	325	330	335	
Phe	Lys	Asn	Met	Val	Phe	Glu	Leu	Pro	Ile	Ile	Gly	Lys	Arg	Lys	Phe	340	345	350	
Leu	Lys	Asp	Ala	Gln	Lys	Ile	Ile	Pro	Ser	Leu	Ser	Leu	Glu	Asp	Leu	355	360	365	
Glu	Tyr	Ala	His	Gly	Phe	Gly	Glu	Val	Arg	Pro	Gln	Val	Leu	Asp	Arg	370	375	380	
Thr	Lys	Arg	Lys	Leu	Glu	Leu	Gly	Glu	Lys	Lys	Ile	Cys	Thr	His	Lys	385	390	395	400
Gly	Ile	Thr	Phe	Asn	Met	Thr	Pro	Ser	Pro	Gly	Ala	Thr	Ser	Cys	Leu	405	410	415	
Gln	Asn	Ala	Leu	Val	Asp	Ser	Gln	Glu	Ile	Ala	Ala	Tyr	Leu	Gly	Glu	420	425	430	
Ser	Phe	Glu	Leu	Glu	Arg	Phe	Tyr	Lys	Asp	Leu	Ser	Pro	Glu	Glu	Leu	435	440	445	

Glu Asn
450

<210> 69
<211> 653
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (63)...(590)

<400> 69
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gc atg cca aaa ccc aag aaa aac acc ctc ccc tgt agc ctt tct gtc 107
Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val
1 5 10 15

aaa atg tct tat ttc atg cgc ttt ctc att aaa tgg cgc acc cgc tct 155
Lys Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser
20 25 30

tta agc cat aaa atg atg act ctc att caa atc tta agc att ctg gct 203
Leu Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala
35 40 45

tta gcg agc aag gcc agt gaa gat tta gaa gag caa ctc aaa aaa atc 251
Leu Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile
50 55 60

aaa gat tac att tat aga acc cta aac gct aaa atc gca tcg gat gtg 299
Lys Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val
65 70 75

tat aac cga gtg ctt att tta gtg aat gaa tat tgc act aat gaa gaa 347
Tyr Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu
80 85 90 95

ttg ttt gac aaa gag agc gtt aaa att tca gat tta ctc att caa gac 395
Leu Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp
100 105 110

att cag ctt tac gct tta gtg gat gaa atg ctt aaa gaa gat aaa tat 443
Ile Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr
115 120 125

caa gtc cag cac acc att tta aag ggc atc atc aaa cgc aaa tac gat 491
Gln Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp
130 135 140

gaa gcc tac tcg ctc aat agc gaa gac agg att ctt tta gaa tac caa 539
Glu Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln
145 150 155

gaa cgc ttg cta gaa cac tca cac gcg tct ttt tca aat aaa aaa ttc 587
Glu Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe
160 165 170 175

aaa tgatttgaaa gcgttacttg ccttgctttt tgggctttta ttgaaaaagg 640
Lys

gcttttaaaat gag 653

<210> 70
<211> 176
<212> PRT
<213> Helicobacter pylori

<400> 70
Met Pro Lys Pro Lys Lys Asn Thr Leu Pro Cys Ser Leu Ser Val Lys
1 5 10 15
Met Ser Tyr Phe Met Arg Phe Leu Ile Lys Trp Arg Thr Arg Ser Leu
20 25 30
Ser His Lys Met Met Thr Leu Ile Gln Ile Leu Ser Ile Leu Ala Leu
35 40 45
Ala Ser Lys Ala Ser Glu Asp Leu Glu Glu Gln Leu Lys Lys Ile Lys
50 55 60
Asp Tyr Ile Tyr Arg Thr Leu Asn Ala Lys Ile Ala Ser Asp Val Tyr
65 70 75 80
Asn Arg Val Leu Ile Leu Val Asn Glu Tyr Cys Thr Asn Glu Glu Leu
85 90 95
Phe Asp Lys Glu Ser Val Lys Ile Ser Asp Leu Leu Ile Gln Asp Ile
100 105 110
Gln Leu Tyr Ala Leu Val Asp Glu Met Leu Lys Glu Asp Lys Tyr Gln
115 120 125
Val Gln His Thr Ile Leu Lys Gly Ile Ile Lys Arg Lys Tyr Asp Glu
130 135 140
Ala Tyr Ser Leu Asn Ser Glu Asp Arg Ile Leu Leu Glu Tyr Gln Glu
145 150 155 160
Arg Leu Leu Glu His Ser His Ala Ser Phe Ser Asn Lys Lys Phe Lys
165 170 175

<210> 71
<211> 1840
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (91)...(1833)

<400> 71
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ttatgaatct cttgtattaa aaggacttca atg aaa aaa ttg gtt tta gtc atc 114
Met Lys Lys Leu Val Leu Val Ile
1 5

ttt tta acg cta gcg ctt tca ata tct gca aaa gaa gtc aaa ata gtg 162
Phe Leu Thr Leu Ala Leu Ser Ile Ser Ala Lys Glu Val Lys Ile Val
10 15 20

ttt tta gaa act tca gac att cat ggg cgg ctt ttt tcg tat gat tat 210
Phe Leu Glu Thr Ser Asp Ile His Gly Arg Leu Phe Ser Tyr Asp Tyr
25 30 35 40

gcg att ggc gag caa aaa ccc aat aac ggc ttg aca agg att gcg act	258
Ala Ile Gly Glu Gln Lys Pro Asn Asn Gly Leu Thr Arg Ile Ala Thr	
45 50 55	
tta atc aaa aag caa agg gct gag aat aaa aat gtg gtt ttg att gac	306
Leu Ile Lys Lys Gln Arg Ala Glu Asn Lys Asn Val Val Leu Ile Asp	
60 65 70	
agc ggg gat ttg ttg caa ggc aat agc gcg gag ttg ttt aat gat gag	354
Ser Gly Asp Leu Leu Gln Gly Asn Ser Ala Glu Leu Phe Asn Asp Glu	
75 80 85	
cca att cat ccg cta gtt aga gct gaa aac gat ttg aaa ttt gac att	402
Pro Ile His Pro Leu Val Arg Ala Glu Asn Asp Leu Lys Phe Asp Ile	
90 95 100	
cgt gtg ctt ggc aat cac gag ttt aat ttc agt aaa gat ttt tta gaa	450
Arg Val Leu Gly Asn His Glu Phe Asn Phe Ser Lys Asp Phe Leu Glu	
105 110 115 120	
aag aat att aag ggg ttt aat ggc gat gtc atg aat gcg aat atc att	498
Lys Asn Ile Lys Gly Phe Asn Gly Asp Val Met Asn Ala Asn Ile Ile	
125 130 135	
aaa att gcg gac aat aag ccg ttt gta aaa cct tat att att aaa aaa	546
Lys Ile Ala Asp Asn Lys Pro Phe Val Lys Pro Tyr Ile Ile Lys Lys	
140 145 150	
att gat ggc gtg agg gtg gcg gtt gtg ggg tat gtg gtg gcg cac atc	594
Ile Asp Gly Val Arg Val Ala Val Val Gly Tyr Val Val Ala His Ile	
155 160 165	
cca act tgg gag gcc tct acg cct gaa cat ttt gca gga ttg aag ttt	642
Pro Thr Trp Glu Ala Ser Thr Pro Glu His Phe Ala Gly Leu Lys Phe	
170 175 180	
ttg gac gct gaa gaa gcg tta aaa aag acc tta aaa gag ttg aaa ggg	690
Leu Asp Ala Glu Glu Ala Leu Lys Lys Thr Leu Lys Glu Leu Lys Gly	
185 190 195 200	
aag tat gat att ttg att ggc gct ttt cat ttg ggg cga gaa gat gag	738
Lys Tyr Asp Ile Leu Ile Gly Ala Phe His Leu Gly Arg Glu Asp Glu	
205 210 215	
aaa ggt ggc gac ggg ata ccg gat tta gcg aaa aaa ttc ccg caa ttt	786
Lys Gly Gly Asp Gly Ile Pro Asp Leu Ala Lys Lys Phe Pro Gln Phe	
220 225 230	
gac atc att ttt gca ggg cat gag cat gcg gtt tat aac acc aaa gta	834
Asp Ile Ile Phe Ala Gly His Glu His Ala Val Tyr Asn Thr Lys Val	
235 240 245	
ggg aaa gtg cat acc att gag cct gga gcg tat ggg gct tat ctg gca	882
Gly Lys Val His Thr Ile Glu Pro Gly Ala Tyr Gly Ala Tyr Leu Ala	
250 255 260	
aag ggc gtg gtg gta ttt gac act aaa acg aag aaa aaa att ata acg	930
Lys Gly Val Val Val Phe Asp Thr Lys Thr Lys Lys Lys Ile Ile Thr	
265 270 275 280	

act gaa aat tta ccc aca aaa gat gtg cca gaa gat gaa gaa tta gcg	978
Thr Glu Asn Leu Pro Thr Lys Asp Val Pro Glu Asp Glu Glu Leu Ala	
285 290 295	
aaa aaa tac gaa tat gtg gat aaa aaa tca aaa gaa tac gct aat gaa	1026
Lys Lys Tyr Glu Tyr Val Asp Lys Lys Ser Lys Glu Tyr Ala Asn Glu	
300 305 310	
gtg gtt ggc gaa gtt aca aaa acc ttt att gac agg cct gat ttt atc	1074
Val Val Gly Glu Val Thr Lys Thr Phe Ile Asp Arg Pro Asp Phe Ile	
315 320 325	
aca gga gaa gaa aaa atc acc acg atg ccc acc gcc gcc ttg caa gaa	1122
Thr Gly Glu Glu Lys Ile Thr Thr Met Pro Thr Ala Ala Leu Gln Glu	
330 335 340	
aca ccg gtg ata gaa ttg att aat aaa gtg caa aaa tat tac gca aaa	1170
Thr Pro Val Ile Glu Leu Ile Asn Lys Val Gln Lys Tyr Tyr Ala Lys	
345 350 355 360	
gcc gat gtt tca gcg gca gcc tta ttc aat ttt ggg gcg aat ttg aaa	1218
Ala Asp Val Ser Ala Ala Ala Leu Phe Asn Phe Gly Ala Asn Leu Lys	
365 370 375	
aaa ggg cct ttc aaa aga aaa gat gtc act tat att tac aag ttc gct	1266
Lys Gly Pro Phe Lys Arg Lys Asp Val Thr Tyr Ile Tyr Lys Phe Ala	
380 385 390	
aat acg ctc att gga gtg cgt ata acg ggt gaa aat ctg ttg aaa tac	1314
Asn Thr Leu Ile Gly Val Arg Ile Thr Gly Glu Asn Leu Leu Lys Tyr	
395 400 405	
atg gaa tgg tca tac cga ttt tac aat cag ttg caa cca gga gat ttg	1362
Met Glu Trp Ser Tyr Arg Phe Tyr Asn Gln Leu Gln Pro Gly Asp Leu	
410 415 420	
acg atc agt ttt aat gaa aac att cgc ggc tat aac ttt gat atg ttt	1410
Thr Ile Ser Phe Asn Glu Asn Ile Arg Gly Tyr Asn Phe Asp Met Phe	
425 430 435 440	
tct ggc gtg aaa tac cag gtt gat gtt aca aaa ccc gcc gga caa agg	1458
Ser Gly Val Lys Tyr Gln Val Asp Val Thr Lys Pro Ala Gly Gln Arg	
445 450 455	
att atc aat ccg aca atc aac aac aaa ccc att gac ccc aaa gcc atc	1506
Ile Ile Asn Pro Thr Ile Asn Asn Lys Pro Ile Asp Pro Lys Ala Ile	
460 465 470	
tat aaa tta gcg atc aac aat tac cga ttc gga aca tta tcc acg aca	1554
Tyr Lys Leu Ala Ile Asn Asn Tyr Arg Phe Gly Thr Leu Ser Thr Thr	
475 480 485	
ttg aat ttg gtt aca gac gct gmt agg tat tat aat tct tac gat gaa	1602
Leu Asn Leu Val Thr Asp Ala Xaa Arg Tyr Tyr Asn Ser Tyr Asp Glu	
490 495 500	
ctg caa gat aat ggg caa ata cga gat ttg atc atc aaa tac atc acg	1650
Leu Gln Asp Asn Gly Gln Ile Arg Asp Leu Ile Ile Lys Tyr Ile Thr	

505	510	515	520	
gaa gaa aaa ggt ggg aag gta acc cct gaa ttg gag ggt aat tgg gaa				1698
Glu Glu Lys Gly Gly Lys Val Thr Pro Glu Leu Glu Gly Asn Trp Glu				
	525	530	535	
atc atc aac tac gat ttc aaa aac ccg ttg ttg gaa aaa ttg aga gaa				1746
Ile Ile Asn Tyr Asp Phe Lys Asn Pro Leu Leu Glu Lys Leu Arg Glu				
	540	545	550	
aaa tta aaa gag ggg agc atc aaa atc ccc acc tca aag gat ggg agg				1794
Lys Leu Lys Glu Gly Ser Ile Lys Ile Pro Thr Ser Lys Asp Gly Arg				
	555	560	565	
act ttg aat gtc aaa tcc att aaa gag agt gaa gtt aaa taaaatt				1840
Thr Leu Asn Val Lys Ser Ile Lys Glu Ser Glu Val Lys				
	570	575	580	

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 <211> 581
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 496
 <223> Xaa= any amino acid

<400> 72

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Ser	Ala	Lys	Glu	Val	Lys	Ile	Val	Phe	Leu	Glu	Thr	Ser	Asp	Ile	His
			20					25					30		
Gly	Arg	Leu	Phe	Ser	Tyr	Asp	Tyr	Ala	Ile	Gly	Glu	Gln	Lys	Pro	Asn
		35					40					45			
Asn	Gly	Leu	Thr	Arg	Ile	Ala	Thr	Leu	Ile	Lys	Lys	Gln	Arg	Ala	Glu
	50					55					60				
Asn	Lys	Asn	Val	Val	Leu	Ile	Asp	Ser	Gly	Asp	Leu	Leu	Gln	Gly	Asn
65					70				75					80	
Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Arg	Ala
			85					90					95		
Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe
			100					105					110		
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly
		115					120					125			
Asp	Val	Met	Asn	Ala	Asn	Ile	Ile	Lys	Ile	Ala	Asp	Asn	Lys	Pro	Phe
	130					135					140				
Val	Lys	Pro	Tyr	Ile	Ile	Lys	Lys	Ile	Asp	Gly	Val	Arg	Val	Ala	Val
145					150				155					160	
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ser	Thr	Pro
			165					170						175	
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Glu	Glu	Ala	Leu	Lys
			180					185					190		
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala
		195					200					205			
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp
	210					215					220				
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu

225					230					235				240
His	Ala	Val	Tyr	Asn	Thr	Lys	Val	Gly	Lys	Val	His	Thr	Ile	Glu
				245					250					255
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp
			260					265					270	
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys
		275					280					285		Asp
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp
	290					295					300			Lys
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys
305					310					315				320
Phe	Ile	Asp	Arg	Pro	Asp	Phe	Ile	Thr	Gly	Glu	Glu	Lys	Ile	Thr
				325					330					335
Met	Pro	Thr	Ala	Ala	Leu	Gln	Glu	Thr	Pro	Val	Ile	Glu	Leu	Ile
			340					345					350	Asn
Lys	Val	Gln	Lys	Tyr	Tyr	Ala	Lys	Ala	Asp	Val	Ser	Ala	Ala	Ala
	355						360					365		Leu
Phe	Asn	Phe	Gly	Ala	Asn	Leu	Lys	Lys	Gly	Pro	Phe	Lys	Arg	Lys
	370				375						380			Asp
Val	Thr	Tyr	Ile	Tyr	Lys	Phe	Ala	Asn	Thr	Leu	Ile	Gly	Val	Arg
385					390					395				400
Thr	Gly	Glu	Asn	Leu	Leu	Lys	Tyr	Met	Glu	Trp	Ser	Tyr	Arg	Phe
			405						410				415	Tyr
Asn	Gln	Leu	Gln	Pro	Gly	Asp	Leu	Thr	Ile	Ser	Phe	Asn	Glu	Asn
		420						425					430	Ile
Arg	Gly	Tyr	Asn	Phe	Asp	Met	Phe	Ser	Gly	Val	Lys	Tyr	Gln	Val
	435					440					445			Asp
Val	Thr	Lys	Pro	Ala	Gly	Gln	Arg	Ile	Ile	Asn	Pro	Thr	Ile	Asn
	450				455					460				Asn
Lys	Pro	Ile	Asp	Pro	Lys	Ala	Ile	Tyr	Lys	Leu	Ala	Ile	Asn	Asn
465					470				475					480
Arg	Phe	Gly	Thr	Leu	Ser	Thr	Thr	Leu	Asn	Leu	Val	Thr	Asp	Ala
			485						490					Xaa
Arg	Tyr	Tyr	Asn	Ser	Tyr	Asp	Glu	Leu	Gln	Asp	Asn	Gly	Gln	Ile
			500					505					510	Arg
Asp	Leu	Ile	Ile	Lys	Tyr	Ile	Thr	Glu	Glu	Lys	Gly	Gly	Lys	Val
	515						520					525		Thr
Pro	Glu	Leu	Glu	Gly	Asn	Trp	Glu	Ile	Ile	Asn	Tyr	Asp	Phe	Lys
	530				535					540				Asn
Pro	Leu	Leu	Glu	Lys	Leu	Arg	Glu	Lys	Leu	Lys	Glu	Gly	Ser	Ile
545					550				555					Lys
Ile	Pro	Thr	Ser	Lys	Asp	Gly	Arg	Thr	Leu	Asn	Val	Lys	Ser	Ile
			565						570					Lys
Glu	Ser	Glu	Val	Lys										
			580											

<210> 73

<211> 1339

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (68)...(1252)

<400> 73

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gttggtta atg gaa tca gta aaa aca gga aaa aca aat aag gtt ggc aag 109

	Met	Glu	Ser	Val	Lys	Thr	Gly	Lys	Thr	Asn	Lys	Val	Gly	Lys		
	1				5					10						
aat	aca	gag	atg	gct	aat	aca	aag	gca	aat	aaa	gag	gct	cat	ttt	aaa	157
Asn	Thr	Glu	Met	Ala	Asn	Thr	Lys	Ala	Asn	Lys	Glu	Ala	His	Phe	Lys	
15					20					25					30	
caa	gcg	agc	acc	att	aca	aat	ata	atc	aga	tca	att	cgt	ggg	att	ttt	205
Gln	Ala	Ser	Thr	Ile	Thr	Asn	Ile	Ile	Arg	Ser	Ile	Arg	Gly	Ile	Phe	
				35					40						45	
aca	aaa	att	gca	aag	aaa	gtt	aga	gga	ctt	gta	aaa	aaa	cac	ccc	aag	253
Thr	Lys	Ile	Ala	Lys	Lys	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	
			50					55					60			
aaa	agc	agt	gcg	gca	tta	gta	gta	ttg	acc	cat	att	gcg	tgc	aag	aaa	301
Lys	Ser	Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	
		65					70					75				
gcg	aaa	gaa	tta	gac	gat	aaa	gtc	caa	gat	aaa	tcc	aaa	caa	gct	gaa	349
Ala	Lys	Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	
	80					85					90					
aaa	gaa	aat	caa	atc	aat	tgg	tgg	aaa	tat	tca	gga	tta	aca	ata	gcg	397
Lys	Glu	Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	
95					100					105					110	
aca	agt	tta	tta	tta	gcc	gct	tgt	agc	act	ggt	gat	gtt	agt	gaa	caa	445
Thr	Ser	Leu	Leu	Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	
				115					120					125		
ata	gaa	cta	gaa	caa	gaa	aaa	caa	aag	acg	agc	aat	ata	gag	act	aac	493
Ile	Glu	Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	
			130					135					140			
aat	caa	ata	aaa	gta	gaa	caa	gaa	aaa	caa	aag	aca	agc	aat	ata	gag	541
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	
			145				150					155				
act	aat	aat	caa	ata	aaa	gta	gaa	caa	gaa	caa	caa	aag	aca	agc	aat	589
Thr	Asn	Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Ser	Asn	
	160					165					170					
aca	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	637
Thr	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	
	175				180					185					190	
aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	ttg	gtt	aaa	gaa	cag	aaa	gat	685
Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	
				195					200					205		
ttg	gtt	aaa	aca	cag	aaa	gat	ttc	att	aaa	tat	gta	gaa	caa	aat	tgc	733
Leu	Val	Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys	
			210					215					220			
caa	gaa	aat	cat	aat	caa	ttc	ttt	att	gaa	aaa	gga	gga	att	aag	gct	781
Gln	Glu	Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala	
		225					230					235				

ggt att ggt ata gaa gta gaa gct gaa tgc aaa acc cct aaa cct gca 829
 Gly Ile Gly Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala
 240 245 250
 aaa acc aat caa acc cct atc cag cca aaa cac ctc cca aac tct aaa 877
 Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys
 255 260 265 270
 caa ccc cgc tct caa aga gga tca aaa gcg caa gag ctt atc gct tat 925
 Gln Pro Arg Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr
 275 280 285
 ttg caa aaa gag cta gaa ttt ctg ccc tat tgc caa aaa gct atc gct 973
 Leu Gln Lys Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala
 290 295 300
 aaa caa gtg gat ttt tac agg cca agt tct atc gct tat tta gaa cta 1021
 Lys Gln Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu
 305 310 315
 gat cct aga gat ttt aag gtt aca gaa gaa tgg caa aaa gaa aat cta 1069
 Asp Pro Arg Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu
 320 325 330
 aaa ata cgc tct aaa gct caa gct aaa atg ctt gaa atg aga aac cca 1117
 Lys Ile Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Asn Pro
 335 340 345 350
 caa gcc cac ctt tca aac tct caa agc ctt ttg ttc gtt caa aaa ata 1165
 Gln Ala His Leu Ser Asn Ser Gln Ser Leu Leu Phe Val Gln Lys Ile
 355 360 365
 ttt gct gat gtt aat aaa gaa ata gaa gca gtt gct aat act gaa aag 1213
 Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu Lys
 370 375 380
 aaa gca gaa aaa gcg ggt tat ggt tat agt aaa agg atg tagcgggtaa 1262
 Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
 385 390 395
 aaacattgca ccaagttttt aattatctgt cggcttttga aaacattttt tatggtagcg 1322
 ttatttgca ataaaag 1339

<210> 74
 <211> 395
 <212> PRT
 <213> *Helicobacter pylori*

<400> 74
 Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr
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 Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Ala His Phe Lys Gln Ala
 20 25 30
 Ser Thr Ile Thr Asn Ile Ile Arg Ser Ile Arg Gly Ile Phe Thr Lys
 35 40 45
 Ile Ala Lys Lys Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser
 50 55 60
 Ser Ala Ala Leu Val Val Thr His Ile Ala Cys Lys Lys Ala Lys
 65 70 75 80

Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	
				85					90					95		
Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser	
			100					105					110			
Leu	Leu	Leu	Ala	Ala	Cys	Ser	Thr	Gly	Asp	Val	Ser	Glu	Gln	Ile	Glu	
		115					120					125				
Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	
	130					135					140					
Ile	Lys	Val	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	
145					150					155					160	
Asn	Gln	Ile	Lys	Val	Glu	Gln	Glu	Gln	Gln	Lys	Thr	Ser	Asn	Thr	Gln	
			165						170					175		
Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	
		180						185					190			
Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	Lys	Glu	Gln	Lys	Asp	Leu	Val	
	195						200					205				
Lys	Thr	Gln	Lys	Asp	Phe	Ile	Lys	Tyr	Val	Glu	Gln	Asn	Cys	Gln	Glu	
	210					215					220					
Asn	His	Asn	Gln	Phe	Phe	Ile	Glu	Lys	Gly	Gly	Ile	Lys	Ala	Gly	Ile	
225					230					235					240	
Gly	Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	
			245						250					255		
Asn	Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	
		260						265					270			
Arg	Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln	
	275						280					285				
Lys	Glu	Leu	Glu	Phe	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	
	290					295					300					
Val	Asp	Phe	Tyr	Arg	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	
305					310					315					320	
Arg	Asp	Phe	Lys	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	
			325						330					335		
Arg	Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asn	Pro	Gln	Ala	
		340						345					350			
His	Leu	Ser	Asn	Ser	Gln	Ser	Leu	Leu	Phe	Val	Gln	Lys	Ile	Phe	Ala	
	355						360					365				
Asp	Val	Asn	Lys	Glu	Ile	Glu	Ala	Val	Ala	Asn	Thr	Glu	Lys	Lys	Ala	
	370					375					380					
Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met						
385					390					395						

<210> 75
 <211> 904
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(864)

<400> 75
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 aggttaaac atg att aaa caa acc ctc atc att ctt gcc cct ttt ttt atc 111
 Met Ile Lys Gln Thr Leu Ile Ile Leu Ala Pro Phe Phe Ile
 1 5 10

gca acg ctg ttg tat ttt tta ggc gca ccg gat ggg tta aga cct aac 159
 Ala Thr Leu Leu Tyr Phe Leu Gly Ala Pro Asp Gly Leu Arg Pro Asn

15	20	25	30	
gct tgg ctt tat ttt tgt att ttc atg ggc atg att ata ggg cta att	207			
Ala Trp Leu Tyr Phe Cys Ile Phe Met Gly Met Ile Ile Gly Leu Ile				
35 40 45				
tta gag ccg gtg cca tca ggt tta ata gcg cta agc gcg tta gtg ctg	255			
Leu Glu Pro Val Pro Ser Gly Leu Ile Ala Leu Ser Ala Leu Val Leu				
50 55 60				
tgt ata gcg tta aaa att gga gcg agc gat aaa gta gcg agc gct aat	303			
Cys Ile Ala Leu Lys Ile Gly Ala Ser Asp Lys Val Ala Ser Ala Asn				
65 70 75				
aag gct att tcg tgg ggt ttg agc ggg tat gcg aat aaa acg gtg tgg	351			
Lys Ala Ile Ser Trp Gly Leu Ser Gly Tyr Ala Asn Lys Thr Val Trp				
80 85 90				
ctt gtg ttt gtc gct ttc att ttg ggt tta ggg tat gaa aaa agc ttg	399			
Leu Val Phe Val Ala Phe Ile Leu Gly Leu Gly Tyr Glu Lys Ser Leu				
95 100 105 110				
tta ggg aaa ccg atc gct ctt tta ctg att agg ttt tta ggg caa acc	447			
Leu Gly Lys Arg Ile Ala Leu Leu Leu Ile Arg Phe Leu Gly Gln Thr				
115 120 125				
cct tta ggt tta ggc tat gcg att ggt ttg agc gaa ttg tgt cta gcc	495			
Pro Leu Gly Leu Gly Tyr Ala Ile Gly Leu Ser Glu Leu Cys Leu Ala				
130 135 140				
cct ttt atc cct agc aac tcc gct aga agt gga ggc ata ctc tat ccc	543			
Pro Phe Ile Pro Ser Asn Ser Ala Arg Ser Gly Gly Ile Leu Tyr Pro				
145 150 155				
atc gtt tca tct atc ccg cct tta atg gga tct act cca aat aat aac	591			
Ile Val Ser Ser Ile Pro Pro Leu Met Gly Ser Thr Pro Asn Asn Asn				
160 165 170				
cct gac aaa atc ggc gcg tat ttg atg tgg gtc gct ttg gct tca act	639			
Pro Asp Lys Ile Gly Ala Tyr Leu Met Trp Val Ala Leu Ala Ser Thr				
175 180 185 190				
tgc atc act tcg tcc atg ttt tta acc gcg ctc gct cct aac ccc cta	687			
Cys Ile Thr Ser Ser Met Phe Leu Thr Ala Leu Ala Pro Asn Pro Leu				
195 200 205				
gca atg gaa atc gct gcc aaa atg ggc gtg aat gaa atc tca tgg ttt	735			
Ala Met Glu Ile Ala Ala Lys Met Gly Val Asn Glu Ile Ser Trp Phe				
210 215 220				
tgc tgg ttt tta gcg ttc ttg cct tgt ggg gtg gtt ttg atc ttg ctt	783			
Ser Trp Phe Leu Ala Phe Leu Pro Cys Gly Val Val Leu Ile Leu Leu				
225 230 235				
gtg cct tta ttg gcg tat aaa acc tgc aaa ccc acc tta aaa ggc tca	831			
Val Pro Leu Leu Ala Tyr Lys Thr Cys Lys Pro Thr Leu Lys Gly Ser				
240 245 250				
aaa gaa gtg agt ttg tgg gcc aaa aaa agg aat tagagggcat ggggaggttt	884			

Lys Glu Val Ser Leu Trp Ala Lys Lys Arg Asn
 255 260 265

tcttttaaag aaattttaat

904

<210> 76
 <211> 265
 <212> PRT
 <213> Helicobacter pylori

<400> 76
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 Leu Leu Tyr Phe Leu Gly Ala Pro Asp Gly Leu Arg Pro Asn Ala Trp
 20 25 30
 Leu Tyr Phe Cys Ile Phe Met Gly Met Ile Ile Gly Leu Ile Leu Glu
 35 40 45
 Pro Val Pro Ser Gly Leu Ile Ala Leu Ser Ala Leu Val Leu Cys Ile
 50 55 60
 Ala Leu Lys Ile Gly Ala Ser Asp Lys Val Ala Ser Ala Asn Lys Ala
 65 70 75 80
 Ile Ser Trp Gly Leu Ser Gly Tyr Ala Asn Lys Thr Val Trp Leu Val
 85 90 95
 Phe Val Ala Phe Ile Leu Gly Leu Gly Tyr Glu Lys Ser Leu Leu Gly
 100 105 110
 Lys Arg Ile Ala Leu Leu Leu Ile Arg Phe Leu Gly Gln Thr Pro Leu
 115 120 125
 Gly Leu Gly Tyr Ala Ile Gly Leu Ser Glu Leu Cys Leu Ala Pro Phe
 130 135 140
 Ile Pro Ser Asn Ser Ala Arg Ser Gly Gly Ile Leu Tyr Pro Ile Val
 145 150 155 160
 Ser Ser Ile Pro Pro Leu Met Gly Ser Thr Pro Asn Asn Asn Pro Asp
 165 170 175
 Lys Ile Gly Ala Tyr Leu Met Trp Val Ala Leu Ala Ser Thr Cys Ile
 180 185 190
 Thr Ser Ser Met Phe Leu Thr Ala Leu Ala Pro Asn Pro Leu Ala Met
 195 200 205
 Glu Ile Ala Ala Lys Met Gly Val Asn Glu Ile Ser Trp Phe Ser Trp
 210 215 220
 Phe Leu Ala Phe Leu Pro Cys Gly Val Val Leu Ile Leu Leu Val Pro
 225 230 235 240
 Leu Leu Ala Tyr Lys Thr Cys Lys Pro Thr Leu Lys Gly Ser Lys Glu
 245 250 255
 Val Ser Leu Trp Ala Lys Lys Arg Asn
 260 265

<210> 77
 <211> 1194
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (152)...(1069)

<400> 77
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 tttgacaata ttatactata ataaccaatt agattgggggt tttactgatt tttctttgtg 120

tgagctttgg cttagttttg taaggaatga g atg ata aag agt tgg act aaa	172
Met Ile Lys Ser Trp Thr Lys	
1 5	
aag tgg ttt ttg att tta ttt tta atg gca agt tgt tcc agt tat ttg	220
Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser Cys Ser Ser Tyr Leu	
10 15 20	
gtg gct aca acc ggt gag aaa tat ttt aaa atg gct act caa gcc ttt	268
Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met Ala Thr Gln Ala Phe	
25 30 35	
aag aga ggg gac tac cat aaa gcg gtg gct ttt tat aag agg agc tgt	316
Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe Tyr Lys Arg Ser Cys	
40 45 50 55	
aat tta agg gtg ggg gtt ggt tgc acg agt tta ggc tct atg tat gaa	364
Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu Gly Ser Met Tyr Glu	
60 65 70	
gat ggc gat ggc gtg gat cag aat att aca aaa gcc gtt ttt tat tac	412
Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys Ala Val Phe Tyr Tyr	
75 80 85	
aga aga ggg tgt aat tta agg aat cat ctc gct tgc gcg agt cta ggc	460
Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala Cys Ala Ser Leu Gly	
90 95 100	
tct atg tat gaa gat ggc gat ggt gtg caa aaa aac ctt cca aag gct	508
Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys Asn Leu Pro Lys Ala	
105 110 115	
atc tat tat tac agg aga ggg tgc cac tta aag ggt ggg gtg agc tgt	556
Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys Gly Gly Val Ser Cys	
120 125 130 135	
ggg agt tta ggt ttt atg tat ttt aat ggc acg ggc gtt aag caa aat	604
Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr Gly Val Lys Gln Asn	
140 145 150	
tat gcc aaa gcc ctt ttt ctt tct aaa tac gct tgc agt ttg aat tac	652
Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala Cys Ser Leu Asn Tyr	
155 160 165	
ggc att agt tgt aac ttt gta ggg tat atg tat agg aac gcc aaa ggc	700
Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr Arg Asn Ala Lys Gly	
170 175 180	
gta cag aag gat ttg aaa aaa gcc ctt gcg aat ttt aaa aga ggg tgc	748
Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn Phe Lys Arg Gly Cys	
185 190 195	
cat ttg aaa gac gga gcg agt tgt gtg agc ttg gga tac atg tat gaa	796
His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu Gly Tyr Met Tyr Glu	
200 205 210 215	
gtc ggt atg gat gtc aaa caa aat gga gag caa gcc ttg aat ctt tat	844
Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln Ala Leu Asn Leu Tyr	
220 225 230	

aaa aag ggt tgt tat tta aaa agg ggg agc ggt tgt cat aat gtg gcg 892
 Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly Cys His Asn Val Ala
 235 240 245
 gtg atg tat tac acc ggt aag ggc gtt cca aag gat tta gat aaa gcc 940
 Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys Asp Leu Asp Lys Ala
 250 255 260
 att tcg tat tat aag aaa ggt tgc act cta ggc ttt agt ggt agc tgt 988
 Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly Phe Ser Gly Ser Cys
 265 270 275
 aaa gtg tta gaa gaa gtg att ggc aag aag tct gat gat ttg caa gat 1036
 Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser Asp Asp Leu Gln Asp
 280 285 290 295
 gac gcg caa aac gac acg caa gat gat atg caa taagttaaag cttatggact 1089
 Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln
 300 305
 aatgattaaa actcatctta tagaaatctt tctactctct tggtatcaaa tagggattaa 1149
 gcgtctctat tgatgggtat tgagactaaa aatctgcaaa tctag 1194

<210> 78
 <211> 306
 <212> PRT
 <213> Helicobacter pylori

<400> 78
 Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
 1 5 10 15
 Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
 20 25 30
 Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val
 35 40 45
 Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr
 50 55 60
 Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile
 65 70 75 80
 Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
 85 90 95
 Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
 100 105 110
 Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
 115 120 125
 Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
 130 135 140
 Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys
 145 150 155 160
 Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
 165 170 175
 Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu
 180 185 190
 Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
 195 200 205
 Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly
 210 215 220
 Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly

225					230					235					240
Ser	Gly	Cys	His	Asn	Val	Ala	Val	Met	Tyr	Tyr	Thr	Gly	Lys	Gly	Val
				245					250					255	
Pro	Lys	Asp	Leu	Asp	Lys	Ala	Ile	Ser	Tyr	Tyr	Lys	Lys	Gly	Cys	Thr
			260					265					270		
Leu	Gly	Phe	Ser	Gly	Ser	Cys	Lys	Val	Leu	Glu	Glu	Val	Ile	Gly	Lys
		275				280					285				
Lys	Ser	Asp	Asp	Leu	Gln	Asp	Asp	Ala	Gln	Asn	Asp	Thr	Gln	Asp	Asp
	290				295						300				
Met	Gln														
305															

<210> 79
 <211> 1001
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (101)...(865)

<400> 79
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 gcgatttttag gtttaatttg agtttttagg agcagttttt atg caa caa gaa gag 115
 Met Gln Gln Glu Glu
 1 5

att ata gag ggt tat tat ggt gct agc aaa ggg ctt aaa aag agc ggt 163
 Ile Ile Glu Gly Tyr Tyr Gly Ala Ser Lys Gly Leu Lys Lys Ser Gly
 10 15 20

att tat gcc aag ctg gat ttt tta cag agc gct acg ggc ttg att tta 211
 Ile Tyr Ala Lys Lys Leu Asp Phe Leu Gln Ser Ala Thr Gly Leu Ile Leu
 25 30 35

gcg ctc ttt atg ata gca cac atg ttt tta gtc tca agt atc ttg att 259
 Ala Leu Phe Met Ile Ala His Met Phe Leu Val Ser Ser Ile Leu Ile
 40 45 50

agc gat gaa gcc atg tat aaa gtg gcg aaa ttt ttt gaa ggg agc ttg 307
 Ser Asp Glu Ala Met Tyr Lys Val Ala Lys Phe Phe Glu Gly Ser Leu
 55 60 65

ttt tta aaa gcg ggc gag ccg gct att gtg agc gtg gtt gca gca ggg 355
 Phe Leu Lys Ala Gly Glu Pro Ala Ile Val Ser Val Val Ala Ala Gly
 70 75 80 85

att att ctt att tta gtc gcg cat gct ttt ttg gcg tta agg aaa ttc 403
 Ile Ile Leu Ile Leu Val Ala His Ala Phe Leu Ala Leu Arg Lys Phe
 90 95 100

cct atc aat tac agg caa tac aag gtt ttt aaa acc cat aag cat ttg 451
 Pro Ile Asn Tyr Arg Gln Tyr Lys Val Phe Lys Thr His Lys His Leu
 105 110 115

atg aaa cat ggc gat acg agc ttg tgg ttt att caa gcc ctc acc ggg 499
 Met Lys His Gly Asp Thr Ser Leu Trp Phe Ile Gln Ala Leu Thr Gly
 120 125 130

ttt gcg atg ttt ttc tta gcg agt atc cac tta ttt gtc atg ctc aca 547
 Phe Ala Met Phe Phe Leu Ala Ser Ile His Leu Phe Val Met Leu Thr
 135 140 145
 gag cct gaa agt att ggg cct cat ggt tca agc tat cgt ttt gta acg 595
 Glu Pro Glu Ser Ile Gly Pro His Gly Ser Ser Tyr Arg Phe Val Thr
 150 155 160 165
 caa aac ttt tgg ctt ttg tat att ttc tta ttg ttt gcc gta gaa ttg 643
 Gln Asn Phe Trp Leu Leu Tyr Ile Phe Leu Leu Phe Ala Val Glu Leu
 170 175 180
 cat ggc tct att ggg ttg tat cgt tta gcg atc aaa tgg ggg ttg ttt 691
 His Gly Ser Ile Gly Leu Tyr Arg Leu Ala Ile Lys Trp Gly Trp Phe
 185 190 195
 aaa aat gtg agc att caa ggt ttg aga aaa gtc aaa tgg gcg atg agc 739
 Lys Asn Val Ser Ile Gln Gly Leu Arg Lys Val Lys Trp Ala Met Ser
 200 205 210
 gtg ttt ttt att gtt tta ggg ctt tgc acc tat ggg gct tac att aaa 787
 Val Phe Phe Ile Val Leu Gly Leu Cys Thr Tyr Gly Ala Tyr Ile Lys
 215 220 225
 aaa ggt tta gaa aat aag gaa aat ggc att aaa acc atg caa gaa gcc 835
 Lys Gly Leu Glu Asn Lys Glu Asn Gly Ile Lys Thr Met Gln Glu Ala
 230 235 240 245
 ata gaa gct gat ggg aaa ttc cac aaa gaa taagggtaga aaatgaaaat 885
 Ile Glu Ala Asp Gly Lys Phe His Lys Glu
 250 255
 aacatattgt gatgcgctaa ttattggagg cggactagct ggggttaaggg ctagtatcgc 945
 atgcaaacaa aagggtttta acaccatcgt tttaagccta gtgcctgtca ggcgtt 1001

<210> 80
 <211> 255
 <212> PRT
 <213> Helicobacter pylori

<400> 80
 Met Gln Gln Glu Glu Ile Ile Glu Gly Tyr Tyr Gly Ala Ser Lys Gly
 1 5 10 15
 Leu Lys Lys Ser Gly Ile Tyr Ala Lys Leu Asp Phe Leu Gln Ser Ala
 20 25 30
 Thr Gly Leu Ile Leu Ala Leu Phe Met Ile Ala His Met Phe Leu Val
 35 40 45
 Ser Ser Ile Leu Ile Ser Asp Glu Ala Met Tyr Lys Val Ala Lys Phe
 50 55 60
 Phe Glu Gly Ser Leu Phe Leu Lys Ala Gly Glu Pro Ala Ile Val Ser
 65 70 75 80
 Val Val Ala Ala Gly Ile Ile Leu Ile Leu Val Ala His Ala Phe Leu
 85 90 95
 Ala Leu Arg Lys Phe Pro Ile Asn Tyr Arg Gln Tyr Lys Val Phe Lys
 100 105 110
 Thr His Lys His Leu Met Lys His Gly Asp Thr Ser Leu Trp Phe Ile
 115 120 125
 Gln Ala Leu Thr Gly Phe Ala Met Phe Phe Leu Ala Ser Ile His Leu

aaa ccc aag cat ttt gaa gaa atg cat ttt gat ttg cat gcg aat aac 495
 Lys Pro Lys His Phe Glu Glu Met His Phe Asp Leu His Ala Asn Asn
 125 130 135
 aaa acg ccc gaa aaa aag cgc gca atc cct ttt gtg tct atg gat aga 543
 Lys Thr Pro Glu Lys Lys Arg Ala Ile Pro Phe Val Ser Met Asp Arg
 140 145 150
 acg cat ggg gtt ttg atg ctc gcc ggt ttt gtt acc ggc atc ttt tct 591
 Thr His Gly Val Leu Met Leu Ala Gly Phe Val Thr Gly Ile Phe Ser
 155 160 165 170
 atc cca cta ggc atg ggt gga ggg att tta atg gtg ccg ttt ttg ggc 639
 Ile Pro Leu Gly Met Gly Gly Gly Ile Leu Met Val Pro Phe Leu Gly
 175 180 185
 tat ttt ttg aaa tac gat tct aaa aaa atc gtg cct ttg ggg cta ttt 687
 Tyr Phe Leu Lys Tyr Asp Ser Lys Lys Ile Val Pro Leu Gly Leu Phe
 190 195 200
 ttt gtg gtg ttc gct tct tta tct ggg gtc atc tct ctt tat aac ggg 735
 Phe Val Val Phe Ala Ser Leu Ser Gly Val Ile Ser Leu Tyr Asn Gly
 205 210 215
 agg gtt ctt gat aat ata agc gtt caa gcg ggg gtg att acc ggc att 783
 Arg Val Leu Asp Asn Ile Ser Val Gln Ala Gly Val Ile Thr Gly Ile
 220 225 230
 gga gcg ttt tta ggc gtg ggc att ggc atc aag ctt atc gct ttg gct 831
 Gly Ala Phe Leu Gly Val Gly Ile Gly Ile Lys Leu Ile Ala Leu Ala
 235 240 245 250
 aat gaa aag gtg cat aaa atc ctg ttg ctc ctt att tat gct tta agc 879
 Asn Glu Lys Val His Lys Ile Leu Leu Leu Ile Tyr Ala Leu Ser
 255 260 265
 att tta gcg act tta cac aag ctc att atg ggg taaatctaaa aacgcttcta 932
 Ile Leu Ala Thr Leu His Lys Leu Ile Met Gly
 270 275
 gggcattttt aaaattaata tcaaagagct ttcaccagca agc 975

<210> 82
 <211> 277
 <212> PRT
 <213> Helicobacter pylori

<400> 82
 Met Glu Glu Ser Thr Ala Phe Ile Leu Ala Leu Val Gly Leu Phe Thr
 1 5 10 15
 Gly Ile Thr Ala Gly Phe Phe Gly Ile Gly Gly Gly Glu Ile Val Val
 20 25 30
 Pro Ser Ala Ile Phe Ala His Phe Ser Tyr Ser His Ala Val Gly Ile
 35 40 45
 Ser Leu Met Gln Met Leu Phe Ser Ser Val Val Gly Ser Ile Ile Asn
 50 55 60
 Tyr Lys Lys Gly Leu Leu Asp Leu Arg Glu Gly Ser Phe Ala Ala Leu
 65 70 75 80

55	60	65	
aac aac aac gca gaa tta acc cag ttt aaa aaa ata ctc cct caa att Asn Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile 70 75 80 85			474
gag caa cgc ttt gaa acg aat aaa aac gct tat agc gtt caa gcc ttg Glu Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu 90 95 100			522
caa gtg tat ttg agt aat gtg ctt tat aac ttg gtt aat aat agt aat Gln Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn 105 110 115			570
aat ggc agt aat aat gga gtc gtt cct gaa tat gta gga att ata aaa Asn Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys 120 125 130			618
gtt ctc tat ggt tct caa aat gaa ttc agt ctc tta gcc acg gag agt Val Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser 135 140 145			666
gtg gtg ctt tta aac gcg ctt aca agg gtg aat ctg gat agt aat tcg Val Val Leu Leu Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser 150 155 160 165			714
gtg ttt tta aaa ggg cta tta gcc caa atg cag ctt ttt aat gac act Val Phe Leu Lys Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr 170 175 180			762
tct tca gca aag cta ggc cag atc gca gaa aac ttg aag aac ggt ggt Ser Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn Leu Lys Asn Gly Gly 185 190 195			810
gca gga tca atg ctc caa aag gat gtg aaa acc atc tcg gat cga atc Ala Gly Ser Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile 200 205 210			858
gct act tac caa gag aat cta aaa cag cta gga ggg atg cta aag aat Ala Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Lys Asn 215 220 225			906
tac gat gaa ccc tac ttg ccc caa ttt ggg cca ggc aca agc tct cag Tyr Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro Gly Thr Ser Ser Gln 230 235 240 245			954
cat ggg gtt att aat ggc ttt ggc att caa gtg ggc tat aag caa ttt His Gly Val Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe 250 255 260			1002
ttt ggg aac aag cgg aat ata ggc tta cga tat tac gct ttc ttt gat Phe Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp 265 270 275			1050
tat ggc ttt acg caa ttg ggc agt ctt agc agc gcc gtt aaa gcg aat Tyr Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser Ala Val Lys Ala Asn 280 285 290			1098
atc ttt act tat ggc gct ggc acg gac ttt tta tgg aat atc ttt aga			1146

Ile	Phe	Thr	Tyr	Gly	Ala	Gly	Thr	Asp	Phe	Leu	Trp	Asn	Ile	Phe	Arg	
295						300					305					
agg	gtt	ttt	agc	gat	cag	tcc	ttg	aat	gtg	ggg	gtg	ttt	ggg	ggc	att	1194
Arg	Val	Phe	Ser	Asp	Gln	Ser	Leu	Asn	Val	Gly	Val	Phe	Gly	Gly	Ile	
310					315					320					325	
caa	ata	gcg	ggt	aac	act	tgg	gat	agc	tct	tta	aga	ggt	caa	att	gaa	1242
Gln	Ile	Ala	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu	Arg	Gly	Gln	Ile	Glu	
				330					335					340		
aac	tcg	ttt	aaa	gaa	tac	ccc	act	ccc	acg	aat	ttc	caa	ttt	ttg	ttt	1290
Asn	Ser	Phe	Lys	Glu	Tyr	Pro	Thr	Pro	Thr	Asn	Phe	Gln	Phe	Leu	Phe	
			345					350					355			
aat	ttg	ggt	tta	agg	gct	cat	ttt	gcc	agc	acc	atg	cac	cgc	cgg	ttt	1338
Asn	Leu	Gly	Leu	Arg	Ala	His	Phe	Ala	Ser	Thr	Met	His	Arg	Arg	Phe	
		360				365						370				
ttg	agc	gcg	tct	caa	agc	att	cag	cat	ggg	atg	gaa	ttt	ggc	gtg	aaa	1386
Leu	Ser	Ala	Ser	Gln	Ser	Ile	Gln	His	Gly	Met	Glu	Phe	Gly	Val	Lys	
	375					380					385					
atc	ccg	gct	atc	aat	caa	agg	tat	ttg	agg	gcc	aat	ggg	gct	gat	gtg	1434
Ile	Pro	Ala	Ile	Asn	Gln	Arg	Tyr	Leu	Arg	Ala	Asn	Gly	Ala	Asp	Val	
390					395				400						405	
gat	tac	agg	cgt	ttg	tat	gcg	ttc	tat	atc	aat	tac	acg	ata	ggt	ttt	1482
Asp	Tyr	Arg	Arg	Leu	Tyr	Ala	Phe	Tyr	Ile	Asn	Tyr	Thr	Ile	Gly	Phe	
				410				415					420			
taagctcttt ttagggctta taaagaggct ttttactttt tttttggtat tctaacaagc 1542 ttttaaataa tccaatctac tttgttttaa ggataatatt ttatggcaga tgctgttggtg 1602 gggatccagt ggggagatga ggggaaggga aaaattgttg ataggatcgc taaagattat 1662 gactt 1667																

<210> 84
<211> 421
<212> PRT
<213> Helicobacter pylori

<400> 84																
Met	Gly	Val	Gly	Tyr	Gln	Ile	Gly	Gly	Ala	Gln	Gln	Asn	Ile	Asp	Asn	
1				5					10					15		
Lys	Gly	Ser	Thr	Leu	Arg	Asn	Asn	Val	Ile	Asn	Asn	Phe	Arg	Gln	Val	
			20					25					30			
Gly	Val	Gly	Met	Ala	Gly	Gly	Asn	Gly	Leu	Leu	Ala	Leu	Ala	Thr	Asn	
		35					40					45				
Thr	Thr	Met	Asp	Ala	Leu	Leu	Gly	Ile	Gly	Asn	Gln	Ile	Val	Asn	Thr	
	50					55					60					
Asn	Thr	Thr	Val	Ser	Asn	Asn	Asn	Ala	Glu	Leu	Thr	Gln	Phe	Lys	Lys	
65					70				75						80	
Ile	Leu	Pro	Gln	Ile	Glu	Gln	Arg	Phe	Glu	Thr	Asn	Lys	Asn	Ala	Tyr	
			85					90						95		
Ser	Val	Gln	Ala	Leu	Gln	Val	Tyr	Leu	Ser	Asn	Val	Leu	Tyr	Asn	Leu	
			100					105					110			
Val	Asn	Asn	Ser	Asn	Asn	Gly	Ser	Asn	Asn	Gly	Val	Val	Pro	Glu	Tyr	
		115				120						125				
Val	Gly	Ile	Ile	Lys	Val	Leu	Tyr	Gly	Ser	Gln	Asn	Glu	Phe	Ser	Leu	

130	135	140
Leu Ala Thr Glu Ser Val	Val Leu Leu Asn Ala	Leu Thr Arg Val Asn
145	150	155
Leu Asp Ser Asn Ser Val	Phe Leu Lys Gly Leu	Leu Ala Gln Met Gln
165	170	175
Leu Phe Asn Asp Thr Ser	Ser Ala Lys Leu Gly	Gln Ile Ala Glu Asn
180	185	190
Leu Lys Asn Gly Gly Ala	Gly Ser Met Leu Gln	Lys Asp Val Lys Thr
195	200	205
Ile Ser Asp Arg Ile Ala	Thr Tyr Gln Glu Asn	Leu Lys Gln Leu Gly
210	215	220
Gly Met Leu Lys Asn Tyr	Asp Glu Pro Tyr Leu	Pro Gln Phe Gly Pro
225	230	235
Gly Thr Ser Ser Gln His	Gly Val Ile Asn Gly	Phe Gly Ile Gln Val
245	250	255
Gly Tyr Lys Gln Phe Phe	Gly Asn Lys Arg Asn	Ile Gly Leu Arg Tyr
260	265	270
Tyr Ala Phe Phe Asp Tyr	Gly Phe Thr Gln Leu	Gly Ser Leu Ser Ser
275	280	285
Ala Val Lys Ala Asn Ile	Phe Thr Tyr Gly Ala	Gly Thr Asp Phe Leu
290	295	300
Trp Asn Ile Phe Arg Arg	Val Phe Ser Asp Gln	Ser Leu Asn Val Gly
305	310	315
Val Phe Gly Gly Ile Gln	Ile Ala Gly Asn Thr	Trp Asp Ser Ser Leu
325	330	335
Arg Gly Gln Ile Glu Asn	Ser Phe Lys Glu Tyr	Pro Thr Pro Thr Asn
340	345	350
Phe Gln Phe Leu Phe Asn	Leu Gly Leu Arg Ala	His Phe Ala Ser Thr
355	360	365
Met His Arg Arg Phe Leu	Ser Ala Ser Gln Ser	Ile Gln His Gly Met
370	375	380
Glu Phe Gly Val Lys Ile	Pro Ala Ile Asn Gln	Arg Tyr Leu Arg Ala
385	390	395
Asn Gly Ala Asp Val Asp	Tyr Arg Arg Leu Tyr	Ala Phe Tyr Ile Asn
405	410	415
Tyr Thr Ile Gly Phe		
420		

<210> 85
 <211> 926
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (207)...(746)

<400> 85
 ccccttaatt gcagatgttt tgcaagaggg attgctgtggc gtctatcatt ctagagagat 60
 agacttttga gaaaaagtgg ttgttttaga cagctgtcaa atccaccaaa aagcgtaaat 120
 gcatttgcaa gaaactttga tgatagaagt ggataggctt gatttttctt tagtggagcg 180
 cttgaacatt ttagcgcgca tggaga atg aaa agc atg cgt ttt agt tac att 233
 Met Lys Ser Met Arg Phe Ser Tyr Ile
 1 5
 gag cca aga gcg aaa tac ctt atc agc aag ctt tct aaa att tgg gtt 281
 Glu Pro Arg Ala Lys Tyr Leu Ile Ser Lys Leu Ser Lys Ile Trp Val
 10 15 20 25

ttt tac att ttt tta tct ttt gtg gta ata ggg ggg tta gtg tgg ttt 329
 Phe Tyr Ile Phe Leu Ser Phe Val Val Ile Gly Gly Leu Val Trp Phe
 30 35 40
 atg cac aac gcc att aaa agc act caa gac aac gcg tcc agt ttg acg 377
 Met His Asn Ala Ile Lys Ser Thr Gln Asp Asn Ala Ser Ser Leu Thr
 45 50 55
 atc caa gaa agg ctc tac cgc cat gaa atc agc cgc tta cag gtt aag 425
 Ile Gln Glu Arg Leu Tyr Arg His Glu Ile Ser Arg Leu Gln Val Lys
 60 65 70
 act gat gaa acc tta aaa ctc att aaa gaa gcc aaa aag cgt ttg aat 473
 Thr Asp Glu Thr Leu Lys Leu Ile Lys Glu Ala Lys Lys Arg Leu Asn
 75 80 85
 tat aac gat gat ata cga gat gtt ttg caa ggg ctt ttg aat att gtg 521
 Tyr Asn Asp Asp Ile Arg Asp Val Leu Gln Gly Leu Leu Asn Ile Val
 90 95 100 105
 ccg gat tcc atc act att aat agc att gaa ata gac cag caa agc gtg 569
 Pro Asp Ser Ile Thr Ile Asn Ser Ile Glu Ile Asp Gln Gln Ser Val
 110 115 120
 gtt gtt agc ggt aaa acc cct tct aaa gaa gcc ttt tat ttt ttg ttt 617
 Val Val Ser Gly Lys Thr Pro Ser Lys Glu Ala Phe Tyr Phe Leu Phe
 125 130 135
 caa aac aaa cta aac ccc atg ttt gat tat tct agg gcg gaa ttt ttc 665
 Gln Asn Lys Leu Asn Pro Met Phe Asp Tyr Ser Arg Ala Glu Phe Phe
 140 145 150
 ccc tta agc gat ggg tgg ttt aat ttt gtc tcc acc aac ttt tct aat 713
 Pro Leu Ser Asp Gly Trp Phe Asn Phe Val Ser Thr Asn Phe Ser Asn
 155 160 165
 tcc tta ctg ata aaa aat ccg gag tct att aaa tgaagccatt gcatttttca 766
 Ser Leu Leu Ile Lys Asn Pro Glu Ser Ile Lys
 170 175 180
 cacctggaca gagagcaatc aggcgatgtg gggtttatca ttaaaaacct cgttttttta 826
 ggggtttttt ccttattggg ttggttgaat accgagtatt ttctatggcc tagcatgctg 886
 gaattaaaaa aaatcctttt agaagaaaat cgtaaaaaaa 926

<210> 86
 <211> 180
 <212> PRT
 <213> Helicobacter pylori

<400> 86
 Met Lys Ser Met Arg Phe Ser Tyr Ile Glu Pro Arg Ala Lys Tyr Leu
 1 5 10 15
 Ile Ser Lys Leu Ser Lys Ile Trp Val Phe Tyr Ile Phe Leu Ser Phe
 20 25 30
 Val Val Ile Gly Gly Leu Val Trp Phe Met His Asn Ala Ile Lys Ser
 35 40 45
 Thr Gln Asp Asn Ala Ser Ser Leu Thr Ile Gln Glu Arg Leu Tyr Arg
 50 55 60

His	Glu	Ile	Ser	Arg	Leu	Gln	Val	Lys	Thr	Asp	Glu	Thr	Leu	Lys	Leu
65					70				75						80
Ile	Lys	Glu	Ala	Lys	Lys	Arg	Leu	Asn	Tyr	Asn	Asp	Asp	Ile	Arg	Asp
				85					90					95	
Val	Leu	Gln	Gly	Leu	Leu	Asn	Ile	Val	Pro	Asp	Ser	Ile	Thr	Ile	Asn
			100					105					110		
Ser	Ile	Glu	Ile	Asp	Gln	Gln	Ser	Val	Val	Val	Ser	Gly	Lys	Thr	Pro
		115					120					125			
Ser	Lys	Glu	Ala	Phe	Tyr	Phe	Leu	Phe	Gln	Asn	Lys	Leu	Asn	Pro	Met
	130					135					140				
Phe	Asp	Tyr	Ser	Arg	Ala	Glu	Phe	Phe	Pro	Leu	Ser	Asp	Gly	Trp	Phe
145					150					155					160
Asn	Phe	Val	Ser	Thr	Asn	Phe	Ser	Asn	Ser	Leu	Leu	Ile	Lys	Asn	Pro
				165					170					175	
Glu	Ser	Ile	Lys												
			180												

<210> 87
 <211> 1440
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (151)...(1299)

<400> 87
 agcacttttcg cttttcattg ttttgatgcg acttctagtt tcaggctttt gcaagtgtta 60
 aacgatgagg tgagcgatgc gtttttaatc atacaagatt ttaaagaaca gcgcattcatt 120
 cataaaatca ttcaaaccga tttcaaacgc atg tgc gtg gtt ttg agc gtg aaa 174
 Met Cys Val Val Leu Ser Val Lys
 1 5

aga	gat	ggt	gaa	aaa	act	tta	gaa	aat	aat	gaa	gaa	aat	aaa	gat	gaa	222
Arg	Asp	Gly	Glu	Lys	Thr	Leu	Glu	Asn	Asn	Glu	Glu	Asn	Lys	Asp	Glu	
	10					15					20					

aag	ctt	att	ttg	att	gat	gaa	ttt	gaa	ggt	tta	gcc	aat	aaa	ttc	att	270
Lys	Leu	Ile	Leu	Ile	Asp	Glu	Phe	Glu	Val	Leu	Ala	Asn	Lys	Phe	Ile	
	25				30					35				40		

tct	cgt	ttg	ccc	aat	atc	cct	agc	acc	cct	aga	gag	ttt	ggg	tta	ggc	318
Ser	Arg	Leu	Pro	Asn	Ile	Pro	Ser	Thr	Pro	Arg	Glu	Phe	Gly	Leu	Gly	
				45					50					55		

aag	ggc	gag	atc	atg	gag	att	gat	gtg	cct	ttt	ggg	agt	att	ttt	gct	366
Lys	Gly	Glu	Ile	Met	Glu	Ile	Asp	Val	Pro	Phe	Gly	Ser	Ile	Phe	Ala	
			60					65					70			

tac	aga	cac	att	ggc	tct	atc	aga	caa	aaa	gaa	tac	agg	att	gta	ggg	414
Tyr	Arg	His	Ile	Gly	Ser	Ile	Arg	Gln	Lys	Glu	Tyr	Arg	Ile	Val	Gly	
		75					80					85				

ctt	tat	cgc	aac	gat	gtt	ttg	ttg	ctc	tcc	act	aaa	tct	tta	gtt	atc	462
Leu	Tyr	Arg	Asn	Asp	Val	Leu	Leu	Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	
		90				95					100					

cag	ccg	cga	gac	att	ctc	tta	gtg	gcg	ggt	aat	ccg	gaa	att	ttg	aat	510
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Gln 105	Pro	Arg	Asp	Ile	Leu 110	Leu	Val	Ala	Gly	Asn 115	Pro	Glu	Ile	Leu	Asn 120	
gcg	gtg	tat	ctt	caa	gtc	aaa	agc	aat	gtg	ggg	cag	ttc	cca	gcc	ccc	558
Ala	Val	Tyr	Leu	Gln 125	Val	Lys	Ser	Asn	Val 130	Gly	Gln	Phe	Pro	Ala 135	Pro	
ttt	ggt	aag	agc	att	tat	tta	tac	att	gat	atg	cgt	ttg	cag	aac	aga	606
Phe	Gly	Lys	Ser 140	Ile	Tyr	Leu	Tyr	Ile 145	Asp	Met	Arg	Leu	Gln 150	Asn	Arg	
aaa	gcg	atg	atg	cgc	gat	gtg	tat	caa	gcc	ttg	ttt	ttg	cac	aaa	cat	654
Lys	Ala	Met 155	Met	Arg	Asp	Val	Tyr 160	Gln	Ala	Leu	Phe	Leu 165	His	Lys	His	
tta	aag	agc	tac	aag	ctc	tac	att	cag	ggt	tta	cac	ccc	act	agc	cct	702
Leu	Lys 170	Ser	Tyr	Lys	Leu	Tyr 175	Ile	Gln	Val	Leu	His 180	Pro	Thr	Ser	Pro	
aag	ttt	tac	cat	aaa	ttt	tta	gcg	cta	gaa	acc	gaa	agc	att	gaa	gtg	750
Lys	Phe	Tyr	His	Lys	Phe 190	Leu	Ala	Leu	Glu	Thr 195	Glu	Ser	Ile	Glu	Val 200	
aat	ttt	gat	ttt	tac	agg	aaa	agt	ttt	atc	caa	aaa	ctc	cat	gaa	gac	798
Asn	Phe	Asp	Phe 205	Tyr	Arg	Lys	Ser	Phe 210	Ile	Gln	Lys	Leu	His	Glu 215	Asp	
cac	cag	aaa	aaa	atg	ggc	cta	atc	gtg	gta	ggc	aga	gag	ctt	ttt	tta	846
His	Gln	Lys 220	Lys	Met	Gly	Leu	Ile 225	Val	Val	Gly	Arg	Glu	Leu 230	Phe	Leu	
tct	aaa	aaa	cac	cga	aag	gcc	ttg	tat	aaa	aca	gcc	acc	cca	ggt	tat	894
Ser	Lys 235	Lys	His	Arg	Lys	Ala	Leu 240	Tyr	Lys	Thr	Ala	Thr 245	Pro	Val	Tyr	
aaa	acc	aac	act	tct	ggc	ttg	tct	aaa	acc	tct	caa	agc	gtg	gtg	gta	942
Lys	Thr 250	Asn	Thr	Ser	Gly	Leu 255	Ser	Lys	Thr	Ser	Gln 260	Ser	Val	Val	Val	
ttg	aat	gaa	agt	ttg	gat	att	aat	gag	gac	atg	tct	tca	gtg	att	ttt	990
Leu	Asn 265	Glu	Ser	Leu	Asp 270	Ile	Asn	Glu	Asp 275	Met	Ser	Ser	Val	Ile	Phe 280	
gat	gtg	tct	atg	caa	atg	gat	ttg	ggc	ttg	ttg	ctc	tat	gat	ttt	gac	1038
Asp	Val	Ser	Met 285	Gln	Met	Asp	Leu	Gly	Leu 290	Leu	Leu	Tyr	Asp	Phe 295	Asp	
cct	aac	aag	cgc	tat	aaa	aac	gag	att	gtc	aat	cat	tat	gaa	aat	tta	1086
Pro	Asn	Lys 300	Arg	Tyr	Lys	Asn	Glu	Ile 305	Val	Asn	His	Tyr	Glu 310	Asn	Leu	
gcc	aac	gcg	ttc	aac	cgc	aag	att	gag	att	ttc	caa	acc	gat	att	aga	1134
Ala	Asn 315	Ala	Phe	Asn	Arg	Lys	Ile 320	Glu	Ile	Phe	Gln	Thr 325	Asp	Ile	Arg	
aat	cct	atc	atg	tat	ctc	aat	tct	tta	aga	aat	ccc	att	ttg	cat	ttc	1182
Asn 330	Pro	Ile	Met	Tyr	Leu	Asn 335	Ser	Leu	Arg	Asn 340	Pro	Ile	Leu	His	Phe	

atg cct ttt gaa gag tgc atc acg cac acg cgc ttt tgg tgg ttt tta 1230
 Met Pro Phe Glu Glu Cys Ile Thr His Thr Arg Phe Trp Trp Phe Leu
 345 350 355 360

tcc act aaa gtg gaa aaa tta gcg ttt tta aac gat gat aac cct caa 1278
 Ser Thr Lys Val Glu Lys Leu Ala Phe Leu Asn Asp Asp Asn Pro Gln
 365 370 375

att ttt atc cct gta gcg gag tgaaagaatg caagaaattt taatcccttt 1329
 Ile Phe Ile Pro Val Ala Glu
 380

aaaagaaaaa aactataaag tgtttttggg ggaactgcct gaaataaaaat tgaaacaaaa 1389
 agccctcatc attagcgata gcacgtagc cgggttgcat ttgcctatt t 1440

<210> 88
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 <212> PRT
 <213> Helicobacter pylori

<400> 88
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 Asn Asn Glu Glu Asn Lys Asp Glu Lys Leu Ile Leu Ile Asp Glu Phe
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 Glu Val Leu Ala Asn Lys Phe Ile Ser Arg Leu Pro Asn Ile Pro Ser
 35 40 45
 Thr Pro Arg Glu Phe Gly Leu Gly Lys Gly Glu Ile Met Glu Ile Asp
 50 55 60
 Val Pro Phe Gly Ser Ile Phe Ala Tyr Arg His Ile Gly Ser Ile Arg
 65 70 75 80
 Gln Lys Glu Tyr Arg Ile Val Gly Leu Tyr Arg Asn Asp Val Leu Leu
 85 90 95
 Leu Ser Thr Lys Ser Leu Val Ile Gln Pro Arg Asp Ile Leu Leu Val
 100 105 110
 Ala Gly Asn Pro Glu Ile Leu Asn Ala Val Tyr Leu Gln Val Lys Ser
 115 120 125
 Asn Val Gly Gln Phe Pro Ala Pro Phe Gly Lys Ser Ile Tyr Leu Tyr
 130 135 140
 Ile Asp Met Arg Leu Gln Asn Arg Lys Ala Met Met Arg Asp Val Tyr
 145 150 155 160
 Gln Ala Leu Phe Leu His Lys His Leu Lys Ser Tyr Lys Leu Tyr Ile
 165 170 175
 Gln Val Leu His Pro Thr Ser Pro Lys Phe Tyr His Lys Phe Leu Ala
 180 185 190
 Leu Glu Thr Glu Ser Ile Glu Val Asn Phe Asp Phe Tyr Arg Lys Ser
 195 200 205
 Phe Ile Gln Lys Leu His Glu Asp His Gln Lys Lys Met Gly Leu Ile
 210 215 220
 Val Val Gly Arg Glu Leu Phe Leu Ser Lys Lys His Arg Lys Ala Leu
 225 230 235 240
 Tyr Lys Thr Ala Thr Pro Val Tyr Lys Thr Asn Thr Ser Gly Leu Ser
 245 250 255
 Lys Thr Ser Gln Ser Val Val Val Leu Asn Glu Ser Leu Asp Ile Asn
 260 265 270
 Glu Asp Met Ser Ser Val Ile Phe Asp Val Ser Met Gln Met Asp Leu
 275 280 285
 Gly Leu Leu Leu Tyr Asp Phe Asp Pro Asn Lys Arg Tyr Lys Asn Glu
 290 295 300

Ile	Val	Asn	His	Tyr	Glu	Asn	Leu	Ala	Asn	Ala	Phe	Asn	Arg	Lys	Ile
305					310					315					320
Glu	Ile	Phe	Gln	Thr	Asp	Ile	Arg	Asn	Pro	Ile	Met	Tyr	Leu	Asn	Ser
				325					330					335	
Leu	Arg	Asn	Pro	Ile	Leu	His	Phe	Met	Pro	Phe	Glu	Glu	Cys	Ile	Thr
			340					345					350		
His	Thr	Arg	Phe	Trp	Trp	Phe	Leu	Ser	Thr	Lys	Val	Glu	Lys	Leu	Ala
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Phe	Leu	Asn	Asp	Asp	Asn	Pro	Gln	Ile	Phe	Ile	Pro	Val	Ala	Glu	
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 <212> DNA
 <213> Helicobacter pylori

<220>
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Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr															
	5					10						15			
ggt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt	152														
Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val															
	20				25			30							
tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa	200														
Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys															
	35			40				45					50		
gct tgt gaa tta aat agt ggt aat gga tgt agg ttt tta ggg gat ttt	248														
Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly Asp Phe															
			55				60					65			
tat gag aat gga aaa tat gta aaa aag gat tta aga aaa gct gct caa	296														
Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala Ala Gln															
	70					75					80				
tac tac tct aaa gct tgt gga tta aat gat caa gat ggg tgt tta ata	344														
Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys Leu Ile															
	85					90				95					
cta gga tat aag caa tat gct ggc aag ggc gta gtc aaa aat gaa aaa	392														
Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn Glu Lys															
	100				105			110							
caa gcg gtg aaa acc ttt gaa aag gct tgt agg tta gga tct gaa gac	440														
Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser Glu Asp															
	115				120			125				130			
gca tgt ggt att tta aac aac tac tagatttgaa ataaatgctg ttttttagct	494														

Ala Cys Gly Ile Leu Asn Asn Tyr
135

ggctttcatg tttttgtaac ccc

517

<210> 90
<211> 138
<212> PRT
<213> Helicobacter pylori

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Tyr Tyr Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser
20 25 30
Leu Val Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu
35 40 45
Ser Lys Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly
50 55 60
Asp Phe Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala
65 70 75 80
Ala Gln Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys
85 90 95
Leu Ile Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn
100 105 110
Glu Lys Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser
115 120 125
Glu Asp Ala Cys Gly Ile Leu Asn Asn Tyr
130 135

<210> 91
<211> 1663
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (68)...(1600)

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aacaaac atg aaa aaa ctt ctt tat acc ata ctc gcg ctt ctt tta atc 109
Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile
1 5 10
ggc ctt tta aca atc tat ctc atc ctt ttt aca gaa tgg ggg aat aag 157
Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys
15 20 25 30
atc atc gct tcg tat ata gag aaa aaa atc aac ccg aac gag cac tac 205
Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr
35 40 45
ttg agc gtt aaa acc ttt aaa ttg aga ttc aac tct ttg gat ttt aaa 253
Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys
50 55 60
gct caa gcc aac gat gat tcc acg ctc att ctt aag ggg gat ttt tca 301

Ala	Gln	Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser		
		65					70					75					
ctt	tta	aag	caa	agc	gta	aat	ttg	aat	tac	cat	ata	gat	att	aaa	gat	349	
Leu	Leu	Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp		
		80				85					90						
tta	cgc	tct	ttc	aaa	gaa	tgg	ata	ccc	tac	cct	tta	agg	ggg	gct	gtt	397	
Leu	Arg	Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val		
		95			100					105					110		
atc	act	tct	ggg	aat	att	aaa	ggg	cat	aga	aaa	gcc	ctt	atg	att	caa	445	
Ile	Thr	Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln		
				115					120					125			
ggc	gtc	tct	aat	gtg	gct	caa	tcc	cac	act	gcc	tac	aat	gcc	ctt	tta	493	
Gly	Val	Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu		
			130					135					140				
gat	gat	ttc	aag	ctt	tct	cgc	tta	aat	ttg	aac	gca	caa	gac	gcc	aat	541	
Asp	Asp	Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn		
		145					150					155					
tta	gaa	gat	ttg	ctt	tat	tta	atc	aat	cgc	ccc	gct	tat	gcg	aac	gca	589	
Leu	Glu	Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala		
	160					165					170						
aaa	gtg	tcc	tta	cag	gcg	gat	ttt	aac	tct	cta	aag	cct	tta	gag	ggg	637	
Lys	Val	Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly		
	175				180					185					190		
cat	ttg	atc	cta	aca	gct	aat	aac	gct	tta	atc	aat	aac	gcc	cta	atc	685	
His	Leu	Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile		
				195					200					205			
aat	caa	att	ttt	cat	tta	aac	ctt	aaa	gac	acg	ctt	gtt	ttc	agc	ctc	733	
Asn	Gln	Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu		
		210						215					220				
tcg	cat	tca	agc	gac	ttt	aaa	gga	aac	aaa	gcc	atc	agc	gat	acc	acc	781	
Ser	His	Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr		
		225					230					235					
ctg	act	agc	cct	tta	gcc	aat	ttc	aaa	gcc	cta	aaa	agc	gaa	tac	ctt	829	
Leu	Thr	Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu		
	240					245					250						
ttc	tct	att	tta	aaa	ctc	aac	gcc	ccc	tac	act	tta	gaa	atc	ccc	aat	877	
Phe	Ser	Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn		
	255				260					265					270		
cta	gcc	aaa	ctc	tat	aac	att	acc	aac	cac	ccc	tta	aaa	ggg	agc	ttg	925	
Leu	Ala	Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu		
				275					280					285			
act	tta	aaa	ggc	gct	ata	gaa	caa	agc	ccc	aaa	ctt	tta	aaa	gtc	agc	973	
Thr	Leu	Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser		
		290						295					300				

ggc cat tca aat tta cta gac ggc gcg ctg gat ttc acg ctt tta aat	1021
Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn	
305 310 315	
aaa gat ttg aaa ggg cgt ttt tcc aat att tcc act tta aaa gct tta	1069
Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu	
320 325 330	
gat tta ttc cat tac cct aag ttt ttc caa tcc gtt gca gac gct aat	1117
Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn	
335 340 345 350	
ttg gat tat gat ctt atc gct aag caa ggc gta ttg aaa gcc cgc cta	1165
Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu	
355 360 365	
aaa aac gca aga ttc ctc aaa aat gca ttc agc gat ttt ctc tac tcc	1213
Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser	
370 375 380	
att tct aaa ttt gat att aca aaa gaa att tat aac gat gcc aat ctg	1261
Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu	
385 390 395	
gta agc caa atc aac cag caa cgc ctg ctc tct gat ctg agt tta aaa	1309
Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys	
400 405 410	
agc ccc aaa acc caa ttg aaa atc cat aac ggt ttg ttg gat tta aac	1357
Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn	
415 420 425 430	
acc aaa caa atg aac atg ctc atg gat gcg gaa att tta aaa ttc att	1405
Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile	
435 440 445	
ttt aaa atg aaa ctt caa ggc aac atg cac cag cca aaa ttt tct ctc	1453
Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu	
450 455 460	
att tta aac gaa aaa gcc att cag caa aac ttg caa caa ggc ttg aaa	1501
Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys	
465 470 475	
gaa atc tta aaa aac gac acc ctt aaa aaa ggt tta gat cat ttg ctt	1549
Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu	
480 485 490	
aaa gat gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt aag ggg ctt	1597
Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu	
495 500 505 510	
ttt taaaaatttt aaaggataga aatggcgac attttagtta gcggggcgac	1650
Phe	
ttcagggttt gga	1663

<210> 92

<211> 511
 <212> PRT
 <213> Helicobacter pylori

<400> 92

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		20						25				30			
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	His	Tyr	Leu	Ser
		35					40					45			
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
	50					55					60				
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65					70					75					80
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
				85					90					95	
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr
			100					105					110		
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val
		115					120					125			
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp
	130					135					140				
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu
145					150					155					160
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val
				165					170					175	
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu
			180					185					190		
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln
		195					200					205			
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His
	210					215					220				
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr
225					230					235					240
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser
				245					250					255	
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala
			260					265					270		
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu
		275					280					285			
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His
	290					295					300				
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp
305					310					315					320
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu
				325					330					335	
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp
			340					345					350		
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn
		355					360					365			
Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser
	370					375					380				
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser
385						390				395					400
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro
				405					410					415	
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys
			420					425					430		

Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys
		435					440					445			
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu
	450				455						460				
Asn	Glu	Lys	Ala	Ile	Gln	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile
465					470				475					480	
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp
			485					490						495	
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe	
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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (292)...(645)

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 ccattgcctct atcacgcctt taaatttaga cttaaccagt tatgatgatt tgaaaagtgt 180
 ggaatcttgg catgagggaa tgttaaagt agtaaaaagc accgcttggc ttttttaggg 240
 ctaattgttg gggttctatt cttcttttagt gcgtgtgagc accgcctgca c atg ggg 297
 Met Gly
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tat tat tca gaa gtt aca ggg gat tat ttg ttc aat tat aat tcc act 345
 Tyr Tyr Ser Glu Val Thr Gly Asp Tyr Leu Phe Asn Tyr Asn Ser Thr
 5 10 15

atc gtg gtg gct tat gac aga agc gat gcg atg act tct tat tat atc 393
 Ile Val Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr Tyr Ile
 20 25 30

aat gtg att gtt tat gaa ttg caa aaa tta ggc ttt tac aat gtc ttc 441
 Asn Val Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn Val Phe
 35 40 45 50

acg caa gcg gaa ttc cca cta gat aaa gcc aaa aat gtg atc tat gcg 489
 Thr Gln Ala Glu Phe Pro Leu Asp Lys Ala Lys Asn Val Ile Tyr Ala
 55 60 65

cgc att gtc cgt aac atc tca gct gtg ccg ttc tac caa tac aat tac 537
 Arg Ile Val Arg Asn Ile Ser Ala Val Pro Phe Tyr Gln Tyr Asn Tyr
 70 75 80

caa ctg att gat caa gtc aat aag cct tgt tat ttt ctt ggg ggg cag 585
 Gln Leu Ile Asp Gln Val Asn Lys Pro Cys Tyr Phe Leu Gly Gly Gln
 85 90 95

ttt tat tgc tct caa acc cta cgg att att acg cta tca atg gct tta 633
 Phe Tyr Cys Ser Gln Thr Leu Arg Ile Ile Thr Leu Ser Met Ala Leu
 100 105 110

gcg agc aaa ttt taatgagtgc taattcgcat tttatttttag attggtatga 685

Ala Ser Lys Phe
115

tgtggtgttg caaaaacggg ttttatatgt ggatgggagc gtgagcggga ggacttgccg 745.
ctatcagatg ctgtataggg atttgattaa aagcacgac aaacgcattg attttaaccg 805
ccctgaacgc tactactaca atttaagact gcccctttat cagccatgtt ataggcaatg 865
aatgggttat caggcgattg tatcaatttt gcgctagcca tgtggtgcgc aattgctctt 925
ctttaaaatg cgctcaaaat at 947

<210> 94
<211> 118
<212> PRT

<213> Helicobacter pylori

<400> 94
Met Gly Tyr Tyr Ser Glu Val Thr Gly Asp Tyr Leu Phe Asn Tyr Asn
1 5 10 15
Ser Thr Ile Val Val Ala Tyr Asp Arg Ser Asp Ala Met Thr Ser Tyr
20 25 30
Tyr Ile Asn Val Ile Val Tyr Glu Leu Gln Lys Leu Gly Phe Tyr Asn
35 40 45
Val Phe Thr Gln Ala Glu Phe Pro Leu Asp Lys Ala Lys Asn Val Ile
50 55 60
Tyr Ala Arg Ile Val Arg Asn Ile Ser Ala Val Pro Phe Tyr Gln Tyr
65 70 75 80
Asn Tyr Gln Leu Ile Asp Gln Val Asn Lys Pro Cys Tyr Phe Leu Gly
85 90 95
Gly Gln Phe Tyr Cys Ser Gln Thr Leu Arg Ile Ile Thr Leu Ser Met
100 105 110
Ala Leu Ala Ser Lys Phe
115

<210> 95
<211> 875
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (348)...(716)

<400> 95
tgcggaggga atgtctatga taaaatctca gaaaaatttg tagaaaaagt ggataacggg 60
ttttgaaaat ttttaacctt ttttttatct gtttaaacgc attgttcgcc ctagattcaa 120
acgcacttaa agcagagatt aaagaagttt accttaaaga atacaaagac ttaaaattag 180
aaattgaaac cattaactta gaaatcccag agcgcttttc taacgcttcc attttaagct 240
atgaattaaa cgcttccaat aagcttaaaa aagatggggc cgtgttttta aggttggaag 300
atgatcctaa tttacgcta ccggtgcgtt atagcgtgat aggcagc atg cag gct 356
Met Gln Ala
1
ttt aaa agc gtt agc gcg att aaa aaa gat gaa aac atc acc gct aat 404
Phe Lys Ser Val Ser Ala Ile Lys Lys Asp Glu Asn Ile Thr Ala Asn
5 10 15
aac act caa aaa gag cgc att ttg ttt ggt gcg ctt tct aac ccc tta 452
Asn Thr Gln Lys Glu Arg Ile Leu Phe Gly Ala Leu Ser Asn Pro Leu
20 25 30 35

tta gag ggc gcg att gat aaa gtg agc gcg aaa aat ttt atc ccc cct 500
 Leu Glu Gly Ala Ile Asp Lys Val Ser Ala Lys Asn Phe Ile Pro Pro
 40 45 50

aac acg ctt tta agc acg gat aaa acc caa gct tta att atc gtg cgt 548
 Asn Thr Leu Leu Ser Thr Asp Lys Thr Gln Ala Leu Ile Ile Val Arg
 55 60 65

aaa aat gac att atc acc ggg gtg tat gaa gag ggg caa atc agc ata 596
 Lys Asn Asp Ile Ile Thr Gly Val Tyr Glu Glu Gly Gln Ile Ser Ile
 70 75 80

gaa ata agc cta aaa gcc cta gaa aat ggc gcg ctt aat caa atc att 644
 Glu Ile Ser Leu Lys Ala Leu Glu Asn Gly Ala Leu Asn Gln Ile Ile
 85 90 95

caa gcg aaa aat tta gaa agc aat aaa ata ctc aaa gca aaa gtg ttg 692
 Gln Ala Lys Asn Leu Glu Ser Asn Lys Ile Leu Lys Ala Lys Val Leu
 100 105 110 115

agc agc tct aaa gcg caa atc tta taaaggacat tcatgaaatt ggttttaggc 746
 Ser Ser Ser Lys Ala Gln Ile Leu
 120

atcagtggag cgagcgggat acccctagcc ttgcggtttt tagaaaaatt acccaaagaa 806
 attgaagttt ttgtcgtggc gtctaaaaac gcgcatgtcg tggcgtaga agaataat 866
 attaacctt 875

<210> 96
 <211> 123
 <212> PRT
 <213> Helicobacter pylori

<400> 96
 Met Gln Ala Phe Lys Ser Val Ser Ala Ile Lys Lys Asp Glu Asn Ile
 1 5 10 15
 Thr Ala Asn Asn Thr Gln Lys Glu Arg Ile Leu Phe Gly Ala Leu Ser
 20 25 30
 Asn Pro Leu Leu Glu Gly Ala Ile Asp Lys Val Ser Ala Lys Asn Phe
 35 40 45
 Ile Pro Pro Asn Thr Leu Leu Ser Thr Asp Lys Thr Gln Ala Leu Ile
 50 55 60
 Ile Val Arg Lys Asn Asp Ile Ile Thr Gly Val Tyr Glu Glu Gly Gln
 65 70 75 80
 Ile Ser Ile Glu Ile Ser Leu Lys Ala Leu Glu Asn Gly Ala Leu Asn
 85 90 95
 Gln Ile Ile Gln Ala Lys Asn Leu Glu Ser Asn Lys Ile Leu Lys Ala
 100 105 110
 Lys Val Leu Ser Ser Ser Lys Ala Gln Ile Leu
 115 120

<210> 97
 <211> 394
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (160)...(345)

<400> 97

ggcatcactt ttaacatgac cccttctcca ggcgcgacga gttgtttgca aaacgccctt 60
gtggattccc aagaaatcgc tgcgtatttg ggcgagagct ttgaattaga acgcttttat 120
aaagatttat cccagaaga attggaaaat taaaaacgc atg caa aaa gaa caa 174

Met Gln Lys Glu Gln
1 5

gaa gcc caa gaa atc gct aaa aaa gcc gtt aaa atc gtg ttt ttt tta 222
Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys Ile Val Phe Phe Leu
10 15 20

ggg ctt gtg gtg gtg ctt ttg atg atg ata aac ctt tac atg ctc atc 270
Gly Leu Val Val Val Leu Leu Met Met Ile Asn Leu Tyr Met Leu Ile
25 30 35

aat caa atc aac gcg agc gct caa atg agc cac caa atc aaa aag ata 318
Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His Gln Ile Lys Lys Ile
40 45 50

gaa gaa agg ctt aat cag gag caa aaa taaaaaaggc tttttggtat 365
Glu Glu Arg Leu Asn Gln Glu Gln Lys
55 60

ttttacgatac aaatagtaaa gagcttatac 394

<210> 98

<211> 62

<212> PRT

<213> Helicobacter pylori

<400> 98

Met Gln Lys Glu Gln Glu Ala Gln Glu Ile Ala Lys Lys Ala Val Lys
1 5 10 15
Ile Val Phe Phe Leu Gly Leu Val Val Val Leu Leu Met Met Ile Asn
20 25 30
Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Gln Met Ser His
35 40 45
Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Glu Gln Lys
50 55 60

<210> 99

<211> 516

<212> DNA

<213> Helicobacter pylori

<400> 99

gtttgattta gttcaagagc ttttagaaga atttttgcaa agcggggcta aagagatttt 60
agaaaaggcg cagttgtttt aatgcgtttg tttatcgcg tagttttgtt ttggtggtgg 120
ttaagcttga acgctaaaga agcggatttt atctctgatt tagaatacgg gatggctctt 180
tataaaaacc ctaggggtgt tgcgtgcgcg aaatgccatg gcattaaagg cgaacaacaa 240
gaaatcacct tttattatga aaaaggcgag aaaaaaatcc tctacgcccc taaaatcaac 300
catttggtt ttaaaacctt taaagacgcc ttgagtttag gcaaaggcat gatgcctaaa 360
tacaatctca atttagaaga aatccaagcg atttatcttt atatcatctc tttagagcat 420
aaagaagagc gtaaggattc tcctaagcct taatcaaagc gcttgattta tgctaaaatg 480
gagcgttgca tttttgtttt gattaaagaa gggttc 516

<210> 100
 <211> 709
 <212> DNA
 <213> Helicobacter pylori

<400> 100
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 tgccttgtgt gattagtaac acaaggcaag tgtgataaac cctactacaa tttcaattca 120
 aggagcctaa ctaaaataaa atgaacaatt tcagttaggg ctttattata gcaaaaatta 180
 tctaagatta caaagggtag cgtttctgtt tttggattta gagcgttatt ttgattgttt 240
 tgagtttaat ttactttttg ttttaataata aatcttaact atcataaatg tacaattaaa 300
 gtattttaaaa aaatttttaa acaaaaggat ataaaatgaa aaccattaga aatagcgtgt 360
 ttattggagc gtctttactc ggcggttgcg cttagcgttg ggcttatttt gacgctttgc 420
 atgttgctcg cgtaaagac gcttgtttat agaaaaagaa gcacaccaca cgcccaaaga 480
 ctttgatagc ccttaccaca ctgactaaac cggcactagg ttttagttgg gggtttttag 540
 ggggtgttatt ttagatactc tctgttcctt taaagaaaat aaatttctac cataaaaataa 600
 aatcttaaat taaggcgact aaaacccac ttttaaaaaa ttaaaaagcg ttaagtaaga 660
 cttatccaaa aagcaaagaa aatcaatttt tccaaccact ttttttaag 709

<210> 101
 <211> 33
 <212> DNA
 <213> Helicobacter pylori

<400> 101
 cgcggatccg aaatagggtt gtttttaatt ttc 33

<210> 102
 <211> 30
 <212> DNA
 <213> Helicobacter pylori

<400> 102
 ccgctcgagt taaaaaaga gtttgtataa 30

<210> 103
 <211> 25
 <212> DNA
 <213> Helicobacter pylori

<400> 103
 ggggatcctt ggtagaattg aatca 25

<210> 104
 <211> 23
 <212> DNA
 <213> Helicobacter pylori

<400> 104
 ggaattccta aaacaagaac gcg 23

<210> 105
 <211> 25
 <212> DNA
 <213> Helicobacter pylori

<400> 105
 ggggatcctt ttttcaaaaa caata 25

<210> 106
 <211> 23
 <212> DNA
 <213> Helicobacter pylori

<400> 106
 ggaattctca cattgttttg ctc 23

<210> 107
 <211> 23
 <212> DNA
 <213> Helicobacter pylori

<400> 107
 gcggatccca atttcaaaaa gcc 23

<210> 108
 <211> 25
 <212> DNA
 <213> Helicobacter pylori

<400> 108
 ccgctcgaac taaaaactat aaacg 25

<210> 109
 <211> 32
 <212> DNA
 <213> Helicobacter pylori

<400> 109
 cgcggatccg agattttgaa aggttggtaa tg 32

<210> 110
 <211> 30
 <212> DNA
 <213> Helicobacter pylori

<400> 110
 ccgctcgagc tacatccttt tactataacc 30

<210> 111
 <211> 24
 <212> DNA
 <213> Helicobacter pylori

<400> 111
 gcggatccgg gtattattca gaag 24

<210> 112
 <211> 24
 <212> DNA
 <213> Helicobacter pylori

<400> 112
 ccgctcgagt taaaatttgc tcgc 24